

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 06:01:49 ; Search time 777.143 Seconds
(without alignments)
1462.883 Million cell updates/sec

Title: US-10-661-094-1_COPY_898_917
Perfect score: 20
Sequence: 1 ttcagcgcacatccctcgcgtg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5683141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database : GenEmbl:*
1: gb_da:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_pr:*
8: gb_ro:*
9: gb_ro:*
10: gb_ro:*
11: gb_ro:*
12: gb_ro:*
13: gb_ro:*
14: gb_ro:*
15: gb_ro:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	100.0	20	6 CS061876	CS061876 Sequence
2	100.0	614	1 AT754011	AT754011 Enterococ
3	100.0	1029	6 AR035505	AR035505 Sequence
4	100.0	1029	6 BD181846	BD181846 Polypepti
5	100.0	1032	6 AX085668	AX085668 Sequence
6	100.0	1032	6 AX111560	AX111560 Sequence
7	100.0	1034	6 CQ797595	CQ797595 Sequence
8	100.0	1218	6 AX110332	AX110332 Sequence
9	100.0	1232	6 AX110331	AX110331 Sequence
10	100.0	1237	6 AX110319	AX110319 Sequence
11	100.0	1241	6 AX110316	AX110316 Sequence
12	100.0	1249	6 AX110317	AX110317 Sequence
13	100.0	1263	6 AX110320	AX110320 Sequence
14	100.0	1265	6 AX110323	AX110323 Sequence
15	100.0	1269	6 AX110324	AX110324 Sequence
16	100.0	1272	6 AX110318	AX110318 Sequence
17	100.0	1768	6 EFPVANG	EFPVANG
18	100.0	1768	6 CQ797596	CQ797596 Sequence

19	20	100.0	1768	6 CQ797597	CQ797597 Sequence
20	20	100.0	1768	6 CS061873	CS061873 Sequence
21	20	100.0	1768	6 AX110406	AX110406 Sequence
22	20	100.0	2607	6 AR089411	AR089411 Sequence
23	20	100.0	2607	6 AR093611	AR093611 Sequence
24	20	100.0	2667	6 AR035514	AR035514 Sequence
25	20	100.0	2667	6 BD181855	BD181855 Polypepti
26	20	100.0	3946	6 AX110408	AX110408 Sequence
27	20	100.0	7225	6 AR035512	AR035512 Sequence
28	20	100.0	7225	6 BD181853	BD181853 Polypepti
29	20	100.0	10851	1 TRNVAN	TRNVAN
30	20	100.0	10851	6 AR035513	AR035513 Sequence
31	20	100.0	10851	6 BD181854	BD181854 Polypepti
32	20	100.0	10851	6 AX085648	AX085648 Sequence
33	20	100.0	17510	1 AF516335	AF516335 Enterococ
34	20	100.0	57889	1 AE017171	AE017171 Staphyloc
35	18.4	92.0	786	1 OTEDVANA2	OTEDVANA2
36	18.4	92.0	186605	9 AL606928	AL606928 Mouse DNA
37	18	90.0	339	3 DQ117337	DQ117337 Unculture
38	18	90.0	801	3 AY327227	AY327227 Unculture
39	17.4	87.0	48352	13 AY225134	AY225134 Feldmanni
40	17.4	87.0	92474	8 AC131384	AC131384 Homo sapi
41	17.4	87.0	144542	8 AC015819	AC015819 Homo sapi
42	17.4	87.0	150214	8 AC091489	AC091489 Homo sapi
43	17.4	87.0	153596	14 AC130453	AC130453 Homo sapi
44	17.4	87.0	153773	8 HUAC004020	HUAC004020 Homo sapi
45	17.4	87.0	170711	14 AC032020	AC032020 Homo sapi
46	17.4	87.0	190048	9 AL591126	AL591126 Mouse DNA
47	17.4	87.0	190123	14 AC141358	AC141358 Bos tauri
48	17.4	87.0	203643	14 AC140525	AC140525 Bos tauri
49	17.4	87.0	210236	14 AC150639	AC150639 Bos tauri
50	17.4	87.0	223891	14 AC163846	AC163846 Bos tauri
51	17	85.0	812	15 AJ717397	AJ717397 Schodonor
52	17	85.0	1087	15 AJ717396	AJ717396 Schodonor
53	17	85.0	1087	15 AJ764400	AJ764400 Schodonor
54	17	85.0	1409	15 AY366339	AY366339 Schodonor
55	17	85.0	183689	9 AC138719	AC138719 Mus muscu
56	16.8	84.0	201	10 BV207778	BV207778 eqm2453
57	16.8	84.0	277	3 AF406375	AF406375 Unculture
58	16.8	84.0	304	3 AF640326	AF640326 Unculture
59	16.8	84.0	548	6 BD058535	BD058535 Secreted
60	16.8	84.0	638	6 AX388755	AX388755 Sequence
61	16.8	84.0	1054	1 BCY15704	BCY15704 Bacillus ci
62	16.8	84.0	1107	3 UMBSAR11	UMBSAR11 Unknown mar
63	16.8	84.0	1119	3 AY664069	AY664069 Unculture
64	16.8	84.0	1172	3 AY664067	AY664067 Unculture
65	16.8	84.0	1180	3 AY664079	AY664079 Unculture
66	16.8	84.0	1187	3 AY664092	AY664092 Unculture
67	16.8	84.0	1206	3 AY664083	AY664083 Unculture
68	16.8	84.0	1397	3 DQ071046	DQ071046 Unculture
69	16.8	84.0	1397	3 DQ071146	DQ071146 Unculture
70	16.8	84.0	1397	3 DQ071148	DQ071148 Unculture
71	16.8	84.0	1433	3 AF382131	AF382131 Unculture
72	16.8	84.0	1959	3 DQ009251	DQ009251 Unculture
73	16.8	84.0	2311	8 BC002875	BC002875 Homo sapi
74	16.8	84.0	3121	8 HSU88154	HSU88154 Homo sapien
75	16.8	84.0	3186	8 AY882602	AY882602 Homo sapi
76	16.8	84.0	3211	6 AR077147	AR077147 Sequence
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78	16.8	84.0	3216	6 BC010457	BC010457 Homo sapi
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82	16.8	84.0	3910	6 AR170435	AR170435 Sequence
83	16.8	84.0	3910	6 HSU88153	HSU88153 Homo sapien
84	16.8	84.0	5000	1 ASU13677	ASU13677 Arabidosa sp
85	16.8	84.0	11521	1 AE013459	AE013459 Methanosa
86	16.8	84.0	23152	9 AL731720	AL731720 Mouse DNA
87	16.8	84.0	43190	8 AC005777	AC005777 Homo sapi
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89	16.8	84.0	79995	14 AC022231	AC022231 Mus muscu
90	16.8	84.0	80419	8 AL139826	AL139826 Human DNA
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C 92 16.8 84.0 94023 8 AC008720 Homo sapi
93 16.8 84.0 104771 9 AL603830
94 16.8 84.0 110000 15 BA000819 63
95 16.8 84.0 110000 15 AP008216_130
C 96 16.8 84.0 119227 15 CR378662 M. truncat
97 16.8 84.0 144593 15 AC021891 Genomic S
C 98 16.8 84.0 148671 14 AC120316 Homo sapi
C 99 16.8 84.0 153248 8 AC112191 Homo sapi
C 100 16.8 84.0 154353 8 AC027820 Homo sapi
C 101 16.8 84.0 154405 8 AC004990 Homo sapi
C 102 16.8 84.0 153043 14 AC124654 Homo sapi
C 103 16.8 84.0 166134 9 AC127734 Rattus no
C 104 16.8 84.0 169622 14 AC102421 Mus muscu
105 16.8 84.0 174846 14 AC141676 Apis mell
106 16.8 84.0 191766 8 AC087274 Homo sapi
107 16.8 84.0 192590 14 AC118858 Rattus no
C 108 16.8 84.0 192805 8 AC146435 Pan trogl
C 109 16.8 84.0 192963 14 AC020736 Homo sapi
C 110 16.8 84.0 193896 8 AC048387 Homo sapi
C 111 16.8 84.0 195494 8 AC091153 Homo sapi
C 112 16.8 84.0 197370 14 AC130442 Rattus no
C 113 16.8 84.0 201207 14 AC150689 Bos tauri
C 114 16.8 84.0 204620 9 AC163342 Mus muscu
C 115 16.8 84.0 212749 14 AC156177 Bos tauri
C 116 16.8 84.0 223613 14 AC162216 Rattus no
C 117 16.8 84.0 234160 14 AC117890 Rattus no
C 118 16.8 84.0 241475 14 AC132756 Rattus no
C 119 16.8 84.0 246246 14 AC103121 Rattus no
C 120 16.8 84.0 262124 14 AC095111 Rattus no

ALIGNMENTS

RESULT 1
LOCUS CS061876/c 20 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 4 from Patent WO2005028679.
ACCESSION CS061876
VERSION CS061876.1 GI:62553770

KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Dodgson, K.J.
TITLE Method and kit for identifying vancomycin-resistant enterococcus
JOURNAL Patent: WO 2005028679-A 4 31-MAR-2005;
University of Iowa Research Foundation (US); DODGSON, Kirexy Jane
(US)

FEATURES
source location/Qualifiers
1..20
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/db_xref="taxon:1352"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAGGCTCATCTTCGGTG 20
Db 20 TTGAGGCTCATCTTCGGTG 1

RESULT 2
LOCUS AY754011 614 bp DNA linear BCT 19-JAN-2005
DEFINITION Enterococcus faecium vancomycin resistance protein A (vna) gene,
partial cds.
ACCESSION AY754011

VERSION AY754011.1 GI:57790303
KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1 (bases 1 to 614)
AUTHORS Khudaler, B.Y., Shafiani, S., Tewari, R. and Taneja, N.
TITLE Detection and molecular characterization of vancomycin resistance
genes from clinical strains of Enterococci

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 614)
AUTHORS Khudaler, B.Y., Shafiani, S., Tewari, R. and Taneja, N.
TITLE Direct Submision
JOURNAL Submitted (18-SEP-2004) Biotechnology, Panjab University,
Sector-14, Chandigarh, U.T 160014, India

FEATURES
source location/Qualifiers
1..614
/organism="Enterococcus faecium"
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/db_xref="taxon:1352"

gene <1..>614
/gene="vna"
CDS <1..>614
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/codon_start=1
/transl_table=1
/product="vancomycin resistance protein A"
/protein_id="AAW56079.1"
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/translation="LVKKNHREINHDVAFSAHCKSGEDSGICGLFELSGIPYVC
DIQSSAICMDKSLTYIVANKAGATPAFWINDQDPVATFTYPAFVPAFGSSFG
VKVNSADELDYVIESARQYDSKILIEQAVSGCEVCAVLAGNSAALAVESVDQIRLOX
GIFRIHQEVEPEKSGENAVITVPADLSABERGRIGETAKIKYVAL"

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Query Match 100.0%; Score 20; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAGGCTCATCTTCGGTG 20
Db 288 TTGAGGCTCATCTTCGGTG 307

RESULT 3
LOCUS AR035505 1029 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5871910.
ACCESSION AR035505
VERSION AR035505.1 GI:5952173

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1029)
AUTHORS Arthur, M., Dutka-Malen, S., Molinas, C. and Courvalin, P.
TITLE Probes for the detection of nucleotide sequences implicated in the
expression of resistance to glycopeptides, in particular in
gram-positive bacteria
JOURNAL Patent: US 5871910-A 3 16-FEB-1999;
location/Qualifiers
1..1029
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1029;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAGGCTCATCTTCGGTG 20
Db 1029 TTGAGGCTCATCTTCGGTG 1029

Db 522 TTCAGGCTCATCTTCGGTG 541

RESULT 4
LOCUS BD181846
DEFINITION
1029 bp DNA linear PAT 15-MAY-2003
Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis.

ACCESSION BD181846
VERSION BD181846.1 GI:30792764
KEYWORDS JP 2002320494-A/2.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1029)
AUTHORS Arthur M., Duktamalen, S., Molinas, C. and Courvalin, P.
TITLE glycopeptides implicated in the expression of resistance to polypeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
PATENT: JP 2002320494-A 2 05-NOV-2002;
INSTITUT PASTEUR
COURVALIN

JOURNAL
COMMENT
OS Bacteria
PN JP 2002320494-A/2
PD 05-NOV-2002
PP 21-FEB-2002 JP 2002045484
FR 31-OCT-1990 FR 90/13579
PI MICHEL, ARTHUR, SYLVIE DUKTA-MALEN, CATHERINE MOLINAS, PATRICE COURVALIN

PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10,
PC C12Q1/04, C12Q1/68, G01N33/53, G01N33/566, G01N33/569//C12P21/08, PC (C12Q1/04, C12R1:01), (C12Q1/68, C12N1:01), C12N15/00, C12N5/00 CC Polypeptides implicated in the expression of resistance to CC glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
CC these polypeptides and use for diagnosis
CC Key Location/Qualifiers
FT source 1.1029
FT Location/Qualifiers
1.1029
location/Qualifiers
1.1029
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/organism="unclassified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 522 TTCAGGCTCATCTTCGGTG 541

RESULT 5
LOCUS AX085668
DEFINITION
1032 bp DNA linear PAT 09-MAR-2001
Sequence 21 from Patent WO0112803.
ACCESSION AX085668
VERSION AX085668.1 GI:13275654
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

REFERENCE 1
AUTHORS Inouye, R.T., Torres-Viera, C., Moellerling, R., Gold, H. and Eliopoulos, G.M.
TITLE Methods and compositions for restoring antibiotic susceptibility in glycopeptide-resistant Enterococcus

JOURNAL Patent: WO 0112803-A 21 22-FEB-2001;
Beth Israel Deaconess Medical Center, Inc. (US)
FEATURES
source
1.1032
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/db_xref="taxon:1352"

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Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 522 TTCAGGCTCATCTTCGGTG 541

RESULT 6
LOCUS AX111560
DEFINITION
1032 bp DNA linear PAT 29-MAY-2002
Sequence 2293 from Patent WO0123604.
ACCESSION AX111560
VERSION AX111560.1 GI:13927852
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

REFERENCE 1
AUTHORS Bergeron, M.G., Bolesnot, M., Huletsky, A., m Nard, C., Ouellette, M., Picard, F.J. and Roy, P.H.
TITLE Highly conserved genes and their use to generate probes and primers for detection of microorganisms
PATENT: WO 0123604-A 2293 05-APR-2001;
Intelecto Diagnostico (I.D.I.) INC. (CA)
LOCATION/Qualifiers
1.1032
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/mol_type="unassigned DNA"
/strain="BM4147"
/db_xref="taxon:1352"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1032;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 522 TTCAGGCTCATCTTCGGTG 541

RESULT 7
LOCUS CQ797595
DEFINITION
1034 bp DNA linear PAT 20-APR-2004
Sequence 9 from Patent EP1408120.
ACCESSION CQ797595
VERSION CQ797595.1 GI:46425887
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

REFERENCE 1
AUTHORS Cockerill, F.R. and Sloan, J.M.
TITLE Detection of vancomycin-resistant Enterococcus spp.
PATENT: EP 1408120-A 9 14-APR-2004;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
LOCATION/Qualifiers
1.1034
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/mol_type="unassigned DNA"

ORIGIN /db_xref="taxon:1352"

Query Match 100.0%; Score 20; DB 6; Length 1034;
Best Local Similarity 100.0%; Pred. No. 7.2;
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QY 1 TTCAGGCTCATCCTTCGGTG 20
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Db 522 TTCAGGCTCATCCTTCGGTG 541

RESULT 8 AX110322 1218 bp DNA linear PAT 29-MAY-2002
LOCUS AX110322
DEFINITION Sequence 1055 from Patent WO0123604.
ACCESSION AX110322
VERSION AX110322.1 GI:13926614
KEYWORDS
SOURCE Enterococcus gallinarum
ORGANISM Enterococcus gallinarum
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
PATENT: WO 0123604-A 1055 05-APR-2001;
INfectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source 1. 1218
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/mol_type="unassigned DNA"
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/db_xref="taxon:1352"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCCTTCGGTG 20
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Db 596 TTCAGGCTCATCCTTCGGTG 615

RESULT 9 AX110321 1232 bp DNA linear PAT 29-MAY-2002
LOCUS AX110321
DEFINITION Sequence 1054 from Patent WO0123604.
ACCESSION AX110321
VERSION AX110321.1 GI:13926613
KEYWORDS
SOURCE Enterococcus faecalis
ORGANISM Enterococcus faecalis
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
PATENT: WO 0123604-A 1054 05-APR-2001;
INfectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source 1. 1232
/organism="Enterococcus faecalis"
/mol_type="unassigned DNA"
/db_xref="taxon:1351"
/note="R610"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1232;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCCTTCGGTG 20
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Db 606 TTCAGGCTCATCCTTCGGTG 625

RESULT 10 AX110319 1237 bp DNA linear PAT 29-MAY-2002
LOCUS AX110319
DEFINITION Sequence 1052 from Patent WO0123604.
ACCESSION AX110319
VERSION AX110319.1 GI:13926611
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
PATENT: WO 0123604-A 1052 05-APR-2001;
INfectio Diagnostic (I.D.I.) INC. (CA)
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source 1. 1237
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ORIGIN

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RESULT 11 AX110316 1241 bp DNA linear PAT 29-MAY-2002
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DEFINITION Sequence 1049 from Patent WO0123604.
ACCESSION AX110316
VERSION AX110316.1 GI:13926608
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
PATENT: WO 0123604-A 1049 05-APR-2001;
INfectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source 1. 1241
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 589 TTCAGGCTCATCTTCGGTG 608

RESULT 12
AX110317 1249 bp DNA linear PAT 29-MAY-2002
LOCUS Sequence 1050 from Patent WO0123604.
AX110317
ACCESSION AX110317.1 GI:13926609
VERSION
KEYWORDS
SOURCE Enterococcus gallinarum
ORGANISM Enterococcus gallinarum
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1050 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES Location/Qualifiers
source 1..1249
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/strain="R691"
/db_xref="taxon:1353"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1249;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 618 TTCAGGCTCATCTTCGGTG 637

RESULT 13
AX110320 1263 bp DNA linear PAT 29-MAY-2002
LOCUS Sequence 1053 from Patent WO0123604.
AX110320
ACCESSION AX110320.1 GI:13926612
VERSION
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1053 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES Location/Qualifiers
source 1..1263
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="R581"
/db_xref="taxon:1352"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1263;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 1 TTCAGGCTCATCTTCGGTG 20

Db 610 TTCAGGCTCATCTTCGGTG 629

RESULT 14
AX110323 1265 bp DNA linear PAT 29-MAY-2002
LOCUS Sequence 1056 from Patent WO0123604.
AX110323
ACCESSION AX110323.1 GI:13926615
VERSION
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1056 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES Location/Qualifiers
source 1..1265
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="R688"
/db_xref="taxon:1352"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1265;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 620 TTCAGGCTCATCTTCGGTG 639

RESULT 15
AX110324 1269 bp DNA linear PAT 29-MAY-2002
LOCUS Sequence 1057 from Patent WO0123604.
AX110324
ACCESSION AX110324.1 GI:13926616
VERSION
KEYWORDS
SOURCE Enterococcus flavescens
ORGANISM Enterococcus flavescens
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1057 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES Location/Qualifiers
source 1..1269
/organism="Enterococcus flavescens"
/mol_type="unassigned DNA"
/strain="R689"
/db_xref="taxon:37735"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1269;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 618 TTCAGGCTCATCTTCGGTG 637

RESULT 16
AX110318 1272 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 1051 from Patent WO0123604.
ACCESSION AX110318
VERSION AX110318.1 GI:13926610
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE 1
AUTHORS Bergeron,M.G., Bolesinc,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1051-05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source
1. 1272
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="R481"
/db_xref="taxon:1352"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1272;
Best Local Similarity 100.0%; Pred. No. 7.3; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAGGCTCATCCTTCGGTG 20
Db 598 TTCAGGCTCATCCTTCGGTG 617
RESULT 17
EFPVANAG 1768 bp DNA linear BCT 17-JUN-1991
LOCUS E. faecium plasmid p1816 vana gene for VANA ligase.
DEFINITION X66895
ACCESSION X66895.1 GI:43335
VERSION D-alanyl-D-alanine ligase; VANA glycopeptide resistance protein;
KEYWORDS vancomycin resistance.
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Dutka-Malen,S., Molinas,C., Arthur,M. and Courvalin,P.
TITLE The VANA glycopeptide resistance protein is related to
D-alanyl-D-alanine ligase cell wall biosynthesis enzymes
JOURNAL Mol. Gen. Genet. 224 (3), 364-372 (1990)
PUBMED 2266943
REFERENCE 2 (bases 1 to 1768)
AUTHORS Dutka-Malen,S.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-1991) S. Dutka-Malen, Institut Pasteur, Unile des
Agents Antibacteriens, 28 rue du Dr Roux, Paris Cedex 15, France
FEATURES
source
1. 1768
/organism="Enterococcus faecium"
/mol_type="genomic DNA"
/strain="BM4147"
/db_xref="taxon:1352"
/plasmid="p1816"
/gene="vana"
/gene="vana"
/gene="vana"
/gene="vana"
/codon_start=1
/evidence=experimental
/transl_table=11

/product="VANA ligase"
/protein_id="CAA40215.1"
/db_xref="GI:43336"
/db_xref="GOA:P25051"
/db_xref="UniProt/Swiss-Prot:P25051"
/translation="MRRIRVALLFGCSEEHVSVKSAIEIANKIKCEPELYTIGT
KSGVMRCERPCAEWENDVCYSAVSPDKMFGLLVKRNEYIINKVDVAFSLHCKS
GSDGSIQGFELSGIPVGCIDIOSSAICMDKSLTYIVAKNAGIATPAFVINKDGRPV
AATFTYVPVKPARSGSSFGVKVNSADELDYAIISARQYDSKILIEQAVSGCEVCA
VIGNSALVAVGEIDQRLQYGI FRIHQEYEPKESNAVITVPADLSAERGRIOETA
KIVKALGGRGLARDVMFLQDNGRIYLVNVTLPFTSYSRYPHMAAGIALPELID
RLIVLAKG"
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 1768;
Best Local Similarity 100.0%; Pred. No. 7.4; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAGGCTCATCCTTCGGTG 20
Db 898 TTCAGGCTCATCCTTCGGTG 917
RESULT 18
CQ797596 1768 bp DNA linear PAT 20-APR-2004
LOCUS CQ797596
DEFINITION Sequence 10 from Patent EP1408120.
ACCESSION CQ797596
VERSION CQ797596.1 GI:46425888
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE 1
AUTHORS Cockrell,I.L. and Sloan,L.M.
TITLE Detection of vancomycin-resistant Enterococcus spp
JOURNAL Patent: EP 1408120-A 10 14-APR-2004;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES
source
1. 1768
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/db_xref="taxon:1352"
/note="vana sequence"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 7.4; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAGGCTCATCCTTCGGTG 20
Db 898 TTCAGGCTCATCCTTCGGTG 917
RESULT 19
CQ797597 1768 bp DNA linear PAT 20-APR-2004
LOCUS CQ797597
DEFINITION Sequence 11 from Patent EP1408120.
ACCESSION CQ797597
VERSION CQ797597.1 GI:46425889
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE 1
AUTHORS Cockrell,I.L. and Sloan,L.M.
TITLE Detection of vancomycin-resistant Enterococcus spp
JOURNAL Patent: EP 1408120-A 11 14-APR-2004;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES
location/Qualifiers

source
1. 1768
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/db_xref="taxon:1352"
/note="Vana sequence"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
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898 TTCAGGCTCATCTTCGGTG 917

RESULT 20
CS061873 1768 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 1 from Patent WO2005028679.
ACCESSION CS061873
VERSION CS061873.1 GI:62553767
KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

REFERENCE 1
AUTHORS Dodgson, K.J.
TITLE Method and kit for identifying vancomycin-resistant enterococcus
JOURNAL Patent: WO 2005028679-A 1 31-MAR-2005;
University of Iowa Research Foundation (US); DODGSON, Kirsty Jane (US)

FEATURES
source
1. 1768
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/db_xref="taxon:1352"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
|||||
898 TTCAGGCTCATCTTCGGTG 917

RESULT 21
AX110406 1768 bp DNA linear PAT 29-MAY-2002
LOCUS AX110406
DEFINITION Sequence 1139 from Patent WO0123604.
ACCESSION AX110406
VERSION AX110406.1 GI:13926698
KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

REFERENCE 1
AUTHORS Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M., Picard, P.J., and Roy, P.H.
TITLE Highly conserved genes and their use to generate probes and primers for detection of microorganisms
JOURNAL Infectio Diagnostic (I.D.I.) INC. (CA)
Patent: WO 0123604-A 1139 05-APR-2001;
Location/Qualifiers
1. 1768
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="BM4147"
/db_xref="taxon:1352"
source

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
|||||
898 TTCAGGCTCATCTTCGGTG 917

RESULT 22
AR089411 2607 bp DNA linear PAT 07-SEP-2000
LOCUS AR089411
DEFINITION Sequence 170 from patent US 5994066.
ACCESSION AR089411
VERSION AR089411.1 GI:10016168
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1
AUTHORS Bergeron, M.G., Picard, P.J., Ouellette, M., and Roy, P.H.
TITLE Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 170 30-NOV-1999;
Location/Qualifiers
1. 2607
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2607;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
|||||
1483 TTCAGGCTCATCTTCGGTG 1502

RESULT 23
AR093611 2607 bp DNA linear PAT 08-SEP-2000
LOCUS AR093611
DEFINITION Sequence 170 from patent US 6001564.
ACCESSION AR093611
VERSION AR093611.1 GI:10020360
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1
AUTHORS Bergeron, M.G., Ouellette, M., and Roy, P.H.
TITLE Species specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
JOURNAL Patent: US 6001564-A 170 14-DEC-1999;
Location/Qualifiers
1. 2607
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2607;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
|||||
1483 TTCAGGCTCATCTTCGGTG 1502

RESULT 24
AR035514
LOCUS AR035514 2667 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5871910.
ACCESSION AR035514
VERSION AR035514.1 GI:5952182
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2667)
AUTHORS Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
TITLE Probes for the detection of nucleotide sequences implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria
JOURNAL Patent: US 5871910-A 17 16-FEB-1999;
FEATURES
source Location/Qualifiers
1..2667
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 2667;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 1546 TTCAGGCTCATCTTCGGTG 1565

RESULT 25
BD181855
LOCUS BD181855 2667 bp DNA linear PAT 15-MAY-2003
DEFINITION Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis.
BD181855
ACCESSION BD181855.1 GI:30792773
VERSION JP 2002320494-A/11.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2667)
AUTHORS Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
TITLE Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
JOURNAL Patent: JP 2002320494-A 11 05-NOV-2002;
FEATURES
source Location/Qualifiers
1..2667
/organism="Bacteria".

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 2667;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 1546 TTCAGGCTCATCTTCGGTG 1565

RESULT 26
AX110408
LOCUS AX110408 3946 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 1141 from Patent W00123604.
ACCESSION AX110408
VERSION AX110408.1 GI:13926700
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M., Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1141 05-APR-2001;
FEATURES
source Location/Qualifiers
1..3946
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="BM4147"
/db_xref="taxon:1352"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 3946;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 1483 TTCAGGCTCATCTTCGGTG 1502

RESULT 27
AR035512
LOCUS AR035512 7225 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5871910.
ACCESSION AR035512
VERSION AR035512.1 GI:5952180
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 7225)
AUTHORS Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
TITLE Probes for the detection of nucleotide sequences implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria
JOURNAL Patent: US 5871910-A 15 16-FEB-1999;
FEATURES
source Location/Qualifiers
1..7225
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 7225;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 1483 TTCAGGCTCATCTTCGGTG 1502

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 2667;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 1546 TTCAGGCTCATCTTCGGTG 1565

RESULT 26
AX110408
LOCUS AX110408 3946 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 1141 from Patent W00123604.
ACCESSION AX110408
VERSION AX110408.1 GI:13926700
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M., Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1141 05-APR-2001;
FEATURES
source Location/Qualifiers
1..3946
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="BM4147"
/db_xref="taxon:1352"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 3946;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 1483 TTCAGGCTCATCTTCGGTG 1502

RESULT 27
AR035512
LOCUS AR035512 7225 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5871910.
ACCESSION AR035512
VERSION AR035512.1 GI:5952180
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 7225)
AUTHORS Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
TITLE Probes for the detection of nucleotide sequences implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria
JOURNAL Patent: US 5871910-A 15 16-FEB-1999;
FEATURES
source Location/Qualifiers
1..7225
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 7225;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAGGCTCATCTTCGGTG 20
Db 1483 TTCAGGCTCATCTTCGGTG 1502

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
|||||
5044 TTCAGGCTCATCTTCGGTG 5063

RESULT 28
BD181853

LOCUS
DEFINITION
Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence cod ing for these polypeptides and use for diagnosis.

ACCESSION
BD181853.1 GI:30792771

VERSION
JP 2002320494-A/9.

SOURCE
unidentified

ORGANISM
unclassified.

REFERENCE
1 (bases 1 to 7225)
Arthur, M., Dukarmalen, S., Molinas, C. and Courvaillin, P.
Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence cod ing for these polypeptides and use for diagnosis
Patent: JP 2002320494-A 9 05-NOV-2002;

JOURNAL
INSTITUT PASTEUR

COMMENT
OS Bacteria
PN JP 2002320494-A/9
PD 05-NOV-2002
PF 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PT MICHEL ARTHUR, SYLVIE DUKTA-MALEN, CATHERINE MOLINAS, PATRICE PI
COURVAILLIN
PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10.
PC C1201/04, C1201/66, G01N33/53, G01N33/566, C12P21/08,
PC (C1201/04, C12R1:01), (C1201/66, C12R1:01), C12N15/00, C12N5/00 CC
Polypeptides implicated in the expression of resistance to CC
glycopeptides,
CC in particular in gram-positive bacteria, nucleotide sequence
CC cod ing for
CC these polypeptides and use for diagnosis
FH Key Location/Qualifiers
FT source 1..7225
FT location/Qualifiers
1..7225
/organism="Bacteria".
1..7225
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 7225;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
|||||
5044 TTCAGGCTCATCTTCGGTG 5063

RESULT 29
TRAVAN

LOCUS
DEFINITION
Enterococcus faecium transposon Th1546 transposase, rebo15ase, vanR (vanR), vanS (vanS), vanH (vanH), vanZ (vanZ), vanX (vanX), vanY (vanY), and telcoplanin resistance protein (vanZ) genes, complete cds.

ACCESSION
M97297

VERSION
M97297.1 GI:155036

SOURCE
Enterococcus faecium

ORGANISM
Enterococcus faecium

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
2 (bases 1 to 10851)
Arthur, M., Molinas, C., Depardieu, F. and Courvaillin, P.
Characterization of Th1546, a Tn3-related transposon conferring glycopeptide resistance by synthesis of depsipeptide peptidoglycan precursors in Enterococcus faecium BM4147
J. Bacteriol. 175 (1), 117-127 (1993)

REVIEWED
AUTHORS
TITLE
JOURNAL
PUBMED
7867956

FEATURES
source
1.10851
/organism="Enterococcus faecium"
/mol_type="genomic DNA"
/specimen_voucher="BM4147"
/db_xref="taxon:1352"
/feature_11b="BM 4147"
1..10851
/transposon="Th1546"
1..38
/rpt_type="inverted"
/transposon="Th1546"
complement(75..3041)
/codon_start=1
/transl_table=11
/product="transposase"
/protein_id="AA65951.1"
/db_xref="GI:155037"
/translation="MKIARGHELTPEQRQAQPMQIPDEBNIGTFFTSKDELTIVK
KRREKRLAFVQALVRLPEMPYTHKSIIPSVIQTYSKQIGVSPSSLDHYPERNT
LMDHKEIRSEVDVPTLSEIRNTFKYHLALENGAIHLHCEIDFLAKNKIILP
AITLLEKRWVMEARMAEKLFNTVSKSLINDEKLEKLEGIITSDHSESNKTIILGMLK
PCHSPSEPTFKITLERLEYIRGMDLETVQISLHNRILLOSLRGSRRPEAPAPDFOR
NKRYSITVYIQLTOLITKAPRHHDRILSLSKGRKAOBEIKONKGRKAEKVH
FRTIQALIKAREKLDVYKLSVIERMTFVSVEBAQELARPADYIDLDLQRTY
SLKRTPTLLRLPSTKANEPLOAVETIKGNBSGRKRPDSDPVDTSKRWKH
LYEDDQTYINRYEMAVLTREHVRAGDVSIVSQRYPREBYLPSDDTWNQSKN
TRLSVLSPEYDIERTSSFRERLKLAAANSNKLDGVSLEKGLSLARLEKDVSEAK
KESASLYOQLPRIKLTLMDVAHITGFPHOFTHANSNRKDKKETTIIAALLGMM
NIGLSMAEARPGITQYKLANSCMKRYEDAMKKAQILVNFHKLQLPFTWGDGTT
SSDGMQAGVSLHADNPHYTGKAGATTYPTSDQSSYTYKIIHNSDKALHVD
GLHHTDNLNBEHYTDAGTDQIPGLTHLGFRRPRIDLDSPSKLFTIDKASEYP
KLEALLRGQINTVKYKENYEDVRLAHSIREGVASLIMGLASYSRONSIALALRE
MRERETFIILNYISDSLSRKLORGANGLGAMNGAALAIFFPGQGLREBRTIOHLO
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OLQKVLDDLOSDDIITYTDLRTTRSTQDLPFLINIDKKAASLKLSDTWLDSBN
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SBIADLADIMLPSTGLTICOKIRDKTTPYIMLTGDTGDTATGTLTGADYITK
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YLAHDKTPTLSIIIGYSTLDEAPDMDKXAVHTTLKAYRLQLDPELETRY
NLQITLTAKTIDLYMLVQMTDEFPOLSAHQKQAVIHAEDLTVSGDPAKLARFN
NILENAAVSEDSIIDITAGLSGDVSIFFPKDGLAIPEKFRILNMASS
DMGAGIGLALAEIIVQHGQIYAASNNDYTTFRVLEPAMPOLVVKRS"

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VLGNSALVVEVDQIRLQYGIPIHQEVEPKSENAVITVPADLSAERGGIQA
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RLIVLAKG"

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8016. .8624
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9052. .9963
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SEHNSGLDVGSILTKERAPBEKWIENAMKYGFLIARBEDTETLTGQYEWHLR
YVGLPRLAIKKEKRVLEKYMVLEKKEKITSVSNKGEKELFYYPVATKNTTHVPTML
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10116. .10601
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10116. .10601
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FATGNTREMINNVIIFFPGLLANNFKEIGLPEKPAVLVLSLFEIIQFPAIGA
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TTCAAGCTCATCCTCGGTG 20
Db 7500 TTCAAGCTCATCCTCGGTG 7519

RESULT 30
AR035513
LOCUS
Sequence 16 from patent US 5871910.
DEFINITION
AR035513
VERSION
AR035513.1 GI:5952181
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 10851)
AUTHORS
Arthur M., Dukta-Malen S., Molinas C. and Courvalin P.
TITLE
Probes for the detection of nucleotide sequences implicated in the
expression of resistance to glycopeptides, in particular in
gram-positive bacteria
JOURNAL
Patent: US 5871910-A 16 16-FEB-1999;
FEATURES
source
1. .10851
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 10851;
Best Local Similarity 100.0%; Pred. No. 8.2; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 TTCAAGCTCATCCTCGGTG 20
Db 7500 TTCAAGCTCATCCTCGGTG 7519

RESULT 31
BD181854
LOCUS
DEFINITION
Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence coding for these polypeptides and use for diagnosis.
ACCESSION
BD181854
KEYWORDS
UP 2002320494-A/10.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 10851)
AUTHORS
Arthur M., Dukta-Malen S., Molinas C. and Courvalin P.
TITLE
Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence coding for these polypeptides and use for diagnosis

JOURNAL Patent: JP 200230494-A 10 05-NOV-2002;
INSTITUTE PASTEUR
OS Bacteria
PN JP 200230494-A/10
PD 05-NOV-2002
PF 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PI MICHEL ARTHUR, SYLVIE DURTA-MALEN, CATHERINE MOLINAS, PATRICE PI
COURVALIN
PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12Q1/04, C12Q1/68, G01N33/53, G01N33/566, G01N33/569//C12P21/08,
PC C12Q1/04, C12R1:01, C12Q1/68, C12R1:01, C12N15/00, C12N5/00 CC
Polypeptides implicated in the expression of resistance to CC
glycopeptides,
CC in particular in gram-positive bacteria, nucleotide sequence
CC cod ing for
CC these polypeptides and use for diagnosis
FH key Location/Qualifiers
FT source 1..10851
FT Location/Qualifiers
FT Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAGGCTCATCTTCGGTG 20
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Db 7500 TTCAGGCTCATCTTCGGTG 7519
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RESULT 32
LOCUS AX085648 10851 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 1 from Patent WO0112803.
ACCESSION AX085648
VERSION AX085648.1 GI:13275634
KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE
1 Inouye, R.T., Torres-Viera, C., Moellering, R., Gold, H. and
Blidopoulos, G.M.
Title Methode and compositions for restoring antibiotic susceptibility in
glycopeptide-resistant Enterococcus
Patent: WO 0112803-A 1 22-FEB-2001;
Beth Israel Deaconess Medical Center, Inc. (US)
FEATURES
source 1..10851
Location/Qualifiers
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/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
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Query Match 100.0%; Score 20; DB 6; Length 10851;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAGGCTCATCTTCGGTG 20
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Db 7500 TTCAGGCTCATCTTCGGTG 7519
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RESULT 33
AF516335

LOCUS AF516335 17510 bp DNA linear BCT 28-AUG-2002
DEFINITION Enterococcus faecium plasmid pUW786 multiple antibiotic resistance
gene cluster, complete sequence;
ACCESSION AF516335
VERSION AF516335.1 GI:21886737
KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE
1 (bases 1 to 17510)
Werner, G., Klare, J. and Witte, W.
Title Multi-resistance gene cluster on a plasmid in a clinical isolate of
Enterococcus faecium
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 17510)
Werner, G.
Title Direct Submission
AUTHORS Submitted (29-MAY-2002) Wernigerode Branch, Robert Koch Institute,
Burgstr. 37, Wernigerode 38855, Germany
JOURNAL Location/Qualifiers
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NVRASLYRKLSFVN"
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/db_xref="GI:21886740"
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/transl_table=11
/product="pyruvate dehydrogenase"

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REFERENCE 1 (bases 1 to 57889)
AUTHORS Gill,S., Kolonay,J., Shetty,J., Tenover,F. and Weigel,L.
TITLE Sequence of the Michigan vancomycin-resistant *Staphylococcus aureus* plasmid
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 57889)
AUTHORS Gill,S., Kolonay,J., Shetty,J., Tenover,F. and Weigel,L.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-2003) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
FEATURES
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/protein_id="AAQ17125.1"
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Complement (1885..2307)
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/note="similar to GP:4105402; identified by sequence similarity; putative"
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Complement (2317..2802)
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/note="similar to GP:1383309, and SP:P11045; identified

by sequence similarity; putative"
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/protein_id="AAQ17127.1"
/db_xref="GI:33390921"
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/product="regulator of transfer gene AraA"
/protein_id="AAQ17130.1"
/db_xref="GI:33390924"
/translation="WANNBENSVPFGKKKVSILHLVDPDMKDEIKYAKQKPDVNSQAREILIKGIEQIKSNK"
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/protein_id="AAQ17131.1"

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EDLATSIGLITATLKGNNININVEKRTDNESMTTINEINGSKSEHLISPKOSFIRKA
KEKLTIVSPSRWLFSEFKNSGQIANGFTEFFEARVDESLTENDPVVATKEKYSVSV
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/notes="similar to GP:3676436; identified by sequence
similarity; putative"
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similarity; putative"
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Query Match 100.0%; Score 20; DB 1; Length 57889;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
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Db 34820 TTCAGGCTCATCTTCGGTG 34839

RESULT 35
OTPDVANA2 786 bp DNA linear BCT 18-APR-2005
LOCUS O.tubata plasmid DNA for vancomycin resistance protein.
DEFINITION X79049
ACCESSION X79049.1 GI:479085
VERSION vanA2 gene; vancomycin resistance.
KEYWORDS Oerskovia turbata
SOURCE Oerskovia turbata
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococciaceae; Cellulomonadaceae; Oerskovia.
REFERENCE 1 (bases 1 to 786)
AUTHORS Dutka-Malen S., Molinas C., Arthur M. and Couvreur P.
TITLES The vanA glycopeptide resistance protein is related to
D-alanyl-D-alanine ligase cell wall biosynthesis enzymes
JOURNAL Mol. Gen. Genet. 224 (3), 364-372 (1990)
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PUBMED 2266943
REFERENCE 2
AUTHORS Power, E.G., Abdulla, Y.H., Talaania, H.G., Spice, W., Aathithan, S. and
French, G.L.
TITLE vanA genes in vancomycin-resistant clinical isolates of Oerskovia
JOURNAL turbata and Arcanobacterium (Corynebacterium) haemolyticum
PUBMED 8591934
AUTHORS 3 (bases 1 to 786)
REFERENCE Power, E.G.M.
AUTHORS Direct Submission
JOURNAL Submitted (28-APR-1994) E.G.M. Power, UMDS, Dept of Microbiology,
Guy's Campus, London Bridge, London SE1 9RT, UK
Location/Qualifiers
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NHDVAFSALHKGSGEDSGISGLFELSGIPVGCIDQSSAICMDSKLTIVAKNAGIA
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LIEQAVSGEVCAGVAGNSAALVGEVDQIRIQYGIPIHOBVEPEKSGSENAVITVPA
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361
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/notes="vanA equivalent position 1048"
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ORIGIN
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Best Local Similarity 95.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Oy 1 TTCAGGCTCATCCTTCGGTG 20
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 Db 392 TTCAGGCTCATCCTTCGGTG 411
 |||||

RESULT 36
 AL606928/c 186605 bp DNA linear ROD 16-FEB-2002
 LOCUS Mouse DNA sequence from clone RP23-154F2 on chromosome 3, complete
 DEFINITION sequence.
 AL606928
 ACCESSION AL606928 GI:18855219
 VERSION HTG.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus (house mouse)
 Bkayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1. (bases 1 to 186605)
 Corby, N.
 Direct Submission
 Submitted (16-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Feb 21, 2002 this sequence version replaced gi:117384520.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em, EMBL; Sw,
 SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP
 database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-154F2 is
 from the RPCI-23 Mouse PAC library
 constructed by the group of Pieter de Jong.
 For further details see http://www.chori.org/bacpac/home.htm
 VECTOR: pBlac3.6
 This sequence is the entire insert of clone RP23-154F2. The true
 left end of clone RP23-183J6 is at 140238 in this sequence. The
 true right end of clone RP23-212F17 is at 93544 in this sequence.
 Location/Qualifiers
 1..186605
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /chromosome="3"
 /clone="RP23-154F2"
 /clone_id="RPCI-23"
 4499..4836
 /note="Sequence from overlapping clone RP11-212F17
 (AL583890). Assembly confirmed by restriction digest."
 12403..12687
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 (AL583890). Assembly confirmed by restriction digest."
 77505
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 (AL583890). Assembly confirmed by restriction digest."
 95115
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 be approximately 40bp by restriction digest data."
 183708
 /note="Tandem repeat. Forced join. Gap size estimated to

ORIGIN be approximately 110bp by restriction digest data."
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 Best Local Similarity 95.0%; Pred. No. 76;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TTCAGGCTCATCCTTCGGTG 20
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 Db 181169 TTCAGGCTCATCCTTCGGTG 181150
 |||||

RESULT 37
 DQ117337/c 399 bp DNA linear ENV 04-SEP-2003
 LOCUS Uncultured bacterium clone RS.Muc.107 16S ribosomal RNA gene,
 DEFINITION partial sequence.
 DQ117337
 ACCESSION DQ117337 GI:70672105
 VERSION ENV.
 KEYWORDS uncultured bacterium
 SOURCE uncultured bacterium
 ORGANISM Bacteria; environmental samples.
 1 (bases 1 to 399)
 REFERENCE 1 Kushnaro A., Ben-Dov, E. and Koopman, N.
 TITLE Microbial diversity of Fungia granulosa coral mucus micro-layer
 JOURNAL Unpublished
 2 (bases 1 to 399)
 REFERENCE 2 Kushnaro, A., Ben-Dov, E. and Koopman, N.
 AUTHORS Kushnaro, A., Ben-Dov, E. and Koopman, N.
 TITLE Direct Submission
 JOURNAL Submitted (05-JUL-2005) Biotechnology Engineering, Ben Gurion
 University, P.O.B. 653, Be'er-Sheva 84105, Israel
 Location/Qualifiers
 1..399
 /organism="uncultured bacterium"
 /mol_type="genomic DNA"
 /isolation_source="coral mucus"
 /specific_host="Fungia granulosa"
 /db_xref="taxon:77133"
 /clone="RS.Muc.107"
 /environmental_sample
 /country="Israel; Red Sea"
 <1..>399
 /product="16S ribosomal RNA"

ORIGIN
 Query Match 90.0%; Score 18; DB 3; Length 399;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 CAGGCTCATCCTTCGGTG 20
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 Db 121 CAGGCTCATCCTTCGGTG 104
 |||||

RESULT 38
 AY327227/c 801 bp DNA linear ENV 04-SEP-2003
 LOCUS Uncultured bacterium clone ZB35 16S ribosomal RNA gene, partial
 DEFINITION sequence.
 AY327227
 ACCESSION AY327227 GI:32967957
 VERSION ENV.
 KEYWORDS uncultured bacterium
 SOURCE uncultured bacterium
 ORGANISM Bacteria; environmental samples.
 1 (bases 1 to 801)
 REFERENCE 1 Elshahed, M.S., Senko, J.M., Najjar, F.Z., Kenton, S.M., Roe, B.A.,
 Dewers, T.A., Spear, J.R. and Krumholz, L.R.
 TITLE Bacterial diversity and sulfur cycling in a mesophilic sulfide-rich
 spring
 JOURNAL Appl. Environ. Microbiol. 69 (9), 5609-5621 (2003)
 REFERENCE 2 (bases 1 to 801)

FEATURES	ORIGIN
<p>AUTHORS</p> <p>Elshahed, M.S., Senko, J.M., Nejar, F.Z., Kenton, S.M., Roe, B.A., Dewers, T.A., Spear, J.R. and Krumholz, L.R.</p> <p>TITLE</p> <p>Direct Submission</p> <p>JOURNAL</p> <p>Submitted (20-JUN-2003) Botany and Microbiology, University of Oklahoma, 770 Van Vleet Oval, Norman, OK 73019, USA</p> <p>SOURCE</p> <p>1. .801</p> <p>location/Qualifiers</p>	<p>rRNA</p> <p><1. .>801</p> <p>/product="16S ribosomal RNA"</p>
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<p>RESULT 39</p> <p>LOCUS</p> <p>AY225134</p> <p>DEFINITION</p> <p>Feldmannia irregularis virus a seratin Firtv-1 contig B, partial sequence.</p> <p>ACCESSION</p> <p>AY225134</p> <p>VERSION</p> <p>AY225134.1 GI:38683699</p> <p>KEYWORDS</p> <p>Phycodnaviridae; Phaeovirus.</p> <p>ORGANISM</p> <p>Feldmannia irregularis virus a</p> <p>REFERENCE</p> <p>AUTHORS</p> <p>Delaroque, N., Boland, W., Muller, D.G. and Knippers, R.</p> <p>TITLE</p> <p>Comparisons of two large phaeoviral genomes and evolutionary implications</p> <p>JOURNAL</p> <p>J. Mol. Evol. 57 (6), 613-622 (2003)</p> <p>PUBMED</p> <p>14745530</p> <p>REFERENCE</p> <p>2 (bases 1 to 48352)</p> <p>Delaroque, N., Knippers, R., Mueller, D.G. and Boland, W.</p> <p>AUTHORS</p> <p>Partial Nucleotide Sequence of the Feldmannia irregularis Virus Firtv-1 Genome: On the Evolution of Large Phaeoviral Genomes</p> <p>TITLE</p> <p>Unpublished (2003)</p> <p>JOURNAL</p> <p>3 (bases 1 to 48352)</p> <p>Delaroque, N., Knippers, R., Mueller, D.G. and Boland, W.</p> <p>REFERENCE</p> <p>Direct Submission</p> <p>AUTHORS</p> <p>Submitted (24-JAN-2003) Bioorganics, Max Planck Institute for Chemical Ecology, Winzerstrasse 10, Jena 07745, Germany</p> <p>FEATURES</p> <p>SOURCE</p> <p>1. .48352</p> <p>location/Qualifiers</p>	<p>48352 bp DNA linear VRL 30-JAN-2004</p>
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CDs	mlsc_feature
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PMTKSHDTEVGGMGLAVARLLCRLGSDVLLDOLLEGSTPHAFILKCRISYV
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CDS complement (12075..12596)
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Query Match 87.0%; Score 17.4; DB 13; Length 48352;
Best Local Similarity 94.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCAGGCTCATCTTCGGTG 20
DB 36373 TCAGGCTCATCTTCGGTG 36391

RESULT 40
AC13384/C
LOCUS AC13384 92474 bp DNA linear PRI 24-AUG-2002
DEFINITION Homo sapiens chromosome 16 clone RP11-465L11, complete sequence.
ACCESSION AC13384
KEYWORDS AC13384.1 GI:22380708
SOURCE HTG.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 92474)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratories.
DIRECT SUBMISSION
TITLE Unpublished
2 (bases 1 to 92474)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
DIRECT SUBMISSION
TITLE Submitted (21-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 92474)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
DIRECT SUBMISSION
TITLE Submitted (24-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
Draft Sequence Produced by DOE Joint Genome Institute
WWW.JGI.DOE.GOV
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
WWW.BHGC.STANFORD.EDU
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.3.
NOTES: This is not the entire sequence of the clone (entire
sequence is 163,3kb). It is clipped at the overlap with AC091489.
The number of bases overlapped is 56150.

FEATURES
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ORIGIN
Query Match 87.0%; Score 17.4; DB 8; Length 92474;
Best Local Similarity 94.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCAGGCTCATCTTCGGTG 20
DB 30817 TCAGGCTCATCTTCAGTG 30799

Mon Apr 10 07:41:29 2006

us-10-661-094-1_copy_898_917.rge

Page 18

Search completed: April 9, 2006, 07:14:40
Job time : 784.143 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 05:55:33 ; Search time 381.134 Seconds
(without alignments)
472.135 Million cell updates/sec

Title: US-10-661-094-3

Perfect score: 27
Sequence: 1 cctatcctgttttgttaagccgcgcgc 27

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 333246308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database : N_Geneseq_21.*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001as:*
5: geneseq2001bs:*
6: geneseq2002as:*
7: geneseq2002bs:*
8: geneseq2003as:*
9: geneseq2003bs:*
10: geneseq2003cs:*
11: geneseq2003ds:*
12: geneseq2004as:*
13: geneseq2004bs:*
14: geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	27	100.0	1032	4	AAH02300
4	27	100.0	1218	4	AAH01064
5	27	100.0	1232	4	AAH01063
6	27	100.0	1237	4	AAH01061
7	27	100.0	1241	4	AAH01058
8	27	100.0	1249	4	AAH01059
9	27	100.0	1263	4	AAH01052
10	27	100.0	1265	4	AAH01065
11	27	100.0	1269	4	AAH01066
12	27	100.0	1272	4	AAH01060
13	27	100.0	1768	4	AAH01148
14	27	100.0	1768	12	ADQ47257
15	27	100.0	1768	14	ADY59927
16	27	100.0	2607	2	AAH01150
17	27	100.0	3946	4	AAH01150
18	27	100.0	7227	2	AAQ25183
19	27	100.0	7227	2	AAQ25183

20	27	100.0	10851	2	AAQ25178
21	27	100.0	10851	4	AAH01150
22	20.8	77.0	1071	8	ACA22997
23	20.8	77.0	11000	2	AAH020248 07
24	20.6	76.3	555	12	ADQ47265
25	20.6	76.3	556	12	ADQ47264
26	20.6	76.3	556	12	ADQ47262
27	20.6	76.3	556	12	ADQ47263
28	20.6	76.3	556	12	ADQ47261
29	20.6	76.3	556	12	ADQ47265
30	20.6	76.3	556	12	ADQ47260
31	20.6	76.3	556	12	ADQ47259
32	20.6	76.3	589	2	AAQ69230
33	20.6	76.3	630	14	ADY59941
34	20.6	76.3	783	14	ADY59942
35	20.6	76.3	801	4	AAH01126
36	20.6	76.3	801	14	ADY59937
37	20.6	76.3	801	14	ADY59940
38	20.6	76.3	801	14	ADY59943
39	20.6	76.3	801	14	ADY59939
40	20.6	76.3	801	14	ADY59936
41	20.6	76.3	801	14	ADY59938
42	20.6	76.3	881	12	ADQ47258
43	20.6	76.3	1029	2	AAV37115
44	20.6	76.3	1029	4	AAH02303
45	20.6	76.3	1029	4	AAH01720
46	20.6	76.3	1029	4	AAH01720
47	20.6	76.3	1090	14	ADY59931
48	20.6	76.3	1128	10	ADC90583
49	20.6	76.3	1141	2	AAQ69235
50	20.6	76.3	7160	4	AAH01601
51	20.6	76.3	7678	2	AAH01601
52	20.6	76.3	7678	6	AAH01601
53	19.8	73.3	594	3	AAH01601
54	19.8	73.3	1047	8	ACA8219
55	19.6	72.6	1191	8	ACA82513
56	19.6	72.6	21170	2	AAH020535
57	19.6	72.6	21170	11	AAH020535
58	18.6	68.9	1032	4	AAH01601
59	18.6	68.9	1032	4	AAH01601
60	18.6	68.9	1280	14	AAH01601
61	18.6	68.9	5781	4	AAH01601
62	18.2	67.4	774	5	AAH01601
63	18.2	67.4	819	4	AAH01601
64	18.2	67.4	819	13	ADT48822
65	18.2	67.4	1473	13	ADT48822
66	18.2	67.4	95109	6	AAH01601
67	18.2	67.4	1206	8	ACA45223
68	18.2	67.4	6378	12	ADQ21325
69	18.2	67.4	6378	12	ADQ21325
70	18.2	67.4	6378	12	ADQ21325
71	17.8	65.9	6592	12	ADQ21325
72	17.8	65.9	753	10	ADH01379
73	17.8	65.9	753	10	ADH01379
74	17.8	65.9	1158	10	ADH01379
75	17.8	65.9	1394	5	AAH01601
76	17.8	65.9	2013	13	ADH01379
77	17.8	65.9	2013	13	ADH01379
78	17.8	65.9	88245	13	ADH01379
79	17.8	65.9	88245	13	ADH01379
80	17.8	65.9	121434	12	ADH01379
81	17.8	65.9	121434	14	ADH01379
82	17.8	65.9	251	12	ADQ06948
83	17.6	65.2	251	12	ADQ06948
84	17.6	65.2	263	12	ADQ06948
85	17.6	65.2	263	12	ADQ06948
86	17.6	65.2	268	12	ADQ06948
87	17.6	65.2	273	12	ADQ06948
88	17.6	65.2	277	5	ABV16923
89	17.6	65.2	290	5	ADQ06950
90	17.6	65.2	430	5	ABV16923
91	17.6	65.2	525	11	ACR96095
92	17.6	65.2	943	13	ADH011876

AAQ25178 E. faecium	AAH01150 E. faecium	ACA22997 Prokaryot	ADQ47266 Enterococ	ADQ47264 Enterococ	ADQ47262 E. faecal	ADQ47263 E. faecal	ADQ47261 E. faecal	ADQ47265 E. faecal	ADQ47260 E. faecal	ADQ47259 E. faecal	AAQ69230 Enterococ	ADY59942 Enterococ	ADY59941 Enterococ	ADY59940 Enterococ	ADY59939 Enterococ	ADY59938 Enterococ	ADY59937 Enterococ	ADY59936 Enterococ	ADY59935 Enterococ	ADY59934 Enterococ	ADY59933 Enterococ	ADY59932 Enterococ	ADY59931 Enterococ	ADY59930 Enterococ	ADY59929 Enterococ	ADY59928 Enterococ	ADY59927 Enterococ	ADY59926 Enterococ	ADY59925 Enterococ	ADY59924 Enterococ	ADY59923 Enterococ	ADY59922 Enterococ	ADY59921 Enterococ	ADY59920 Enterococ	ADY59919 Enterococ	ADY59918 Enterococ	ADY59917 Enterococ	ADY59916 Enterococ	ADY59915 Enterococ	ADY59914 Enterococ	ADY59913 Enterococ	ADY59912 Enterococ	ADY59911 Enterococ	ADY59910 Enterococ	ADY59909 Enterococ	ADY59908 Enterococ	ADY59907 Enterococ	ADY59906 Enterococ	ADY59905 Enterococ	ADY59904 Enterococ	ADY59903 Enterococ	ADY59902 Enterococ	ADY59901 Enterococ	ADY59900 Enterococ	ADY59899 Enterococ	ADY59898 Enterococ	ADY59897 Enterococ	ADY59896 Enterococ	ADY59895 Enterococ	ADY59894 Enterococ	ADY59893 Enterococ	ADY59892 Enterococ	ADY59891 Enterococ	ADY59890 Enterococ	ADY59889 Enterococ	ADY59888 Enterococ	ADY59887 Enterococ	ADY59886 Enterococ	ADY59885 Enterococ	ADY59884 Enterococ	ADY59883 Enterococ	ADY59882 Enterococ	ADY59881 Enterococ	ADY59880 Enterococ	ADY59879 Enterococ	ADY59878 Enterococ	ADY59877 Enterococ	ADY59876 Enterococ	ADY59875 Enterococ	ADY59874 Enterococ	ADY59873 Enterococ	ADY59872 Enterococ	ADY59871 Enterococ	ADY59870 Enterococ	ADY59869 Enterococ	ADY59868 Enterococ	ADY59867 Enterococ	ADY59866 Enterococ	ADY59865 Enterococ	ADY59864 Enterococ	ADY59863 Enterococ	ADY59862 Enterococ	ADY59861 Enterococ	ADY59860 Enterococ	ADY59859 Enterococ	ADY59858 Enterococ	ADY59857 Enterococ	ADY59856 Enterococ	ADY59855 Enterococ	ADY59854 Enterococ	ADY59853 Enterococ	ADY59852 Enterococ	ADY59851 Enterococ	ADY59850 Enterococ	ADY59849 Enterococ	ADY59848 Enterococ	ADY59847 Enterococ	ADY59846 Enterococ	ADY59845 Enterococ	ADY59844 Enterococ	ADY59843 Enterococ	ADY59842 Enterococ	ADY59841 Enterococ	ADY59840 Enterococ	ADY59839 Enterococ	ADY59838 Enterococ	ADY59837 Enterococ	ADY59836 Enterococ	ADY59835 Enterococ	ADY59834 Enterococ	ADY59833 Enterococ	ADY59832 Enterococ	ADY59831 Enterococ	ADY59830 Enterococ	ADY59829 Enterococ	ADY59828 Enterococ	ADY59827 Enterococ	ADY59826 Enterococ	ADY59825 Enterococ	ADY59824 Enterococ	ADY59823 Enterococ	ADY59822 Enterococ	ADY59821 Enterococ	ADY59820 Enterococ	ADY59819 Enterococ	ADY59818 Enterococ	ADY59817 Enterococ	ADY59816 Enterococ	ADY59815 Enterococ	ADY59814 Enterococ	ADY59813 Enterococ	ADY59812 Enterococ	ADY59811 Enterococ	ADY59810 Enterococ	ADY59809 Enterococ	ADY59808 Enterococ	ADY59807 Enterococ	ADY59806 Enterococ	ADY59805 Enterococ	ADY59804 Enterococ	ADY59803 Enterococ	ADY59802 Enterococ	ADY59801 Enterococ	ADY59800 Enterococ	ADY59799 Enterococ	ADY59798 Enterococ	ADY59797 Enterococ	ADY59796 Enterococ	ADY59795 Enterococ	ADY59794 Enterococ	ADY59793 Enterococ	ADY59792 Enterococ	ADY59791 Enterococ	ADY59790 Enterococ	ADY59789 Enterococ	ADY59788 Enterococ	ADY59787 Enterococ	ADY59786 Enterococ	ADY59785 Enterococ	ADY59784 Enterococ	ADY59783 Enterococ	ADY59782 Enterococ	ADY59781 Enterococ	ADY59780 Enterococ	ADY59779 Enterococ	ADY59778 Enterococ	ADY59777 Enterococ	ADY59776 Enterococ	ADY59775 Enterococ	ADY59774 Enterococ	ADY59773 Enterococ	ADY59772 Enterococ	ADY59771 Enterococ	ADY59770 Enterococ	ADY59769 Enterococ	ADY59768 Enterococ	ADY59767 Enterococ	ADY59766 Enterococ	ADY59765 Enterococ	ADY59764 Enterococ	ADY59763 Enterococ	ADY59762 Enterococ	ADY59761 Enterococ	ADY59760 Enterococ	ADY59759 Enterococ	ADY59758 Enterococ	ADY59757 Enterococ	ADY59756 Enterococ	ADY59755 Enterococ	ADY59754 Enterococ	ADY59753 Enterococ	ADY59752 Enterococ	ADY59751 Enterococ	ADY59750 Enterococ	ADY59749 Enterococ	ADY59748 Enterococ	ADY59747 Enterococ	ADY59746 Enterococ	ADY59745 Enterococ	ADY59744 Enterococ	ADY59743 Enterococ	ADY59742 Enterococ	ADY59741 Enterococ	ADY59740 Enterococ	ADY59739 Enterococ	ADY59738 Enterococ	ADY59737 Enterococ	ADY59736 Enterococ	ADY59735 Enterococ	ADY59734 Enterococ	ADY59733 Enterococ	ADY59732 Enterococ	ADY59731 Enterococ	ADY59730 Enterococ	ADY59729 Enterococ	ADY59728 Enterococ	ADY59727 Enterococ	ADY59726 Enterococ	ADY59725 Enterococ	ADY59724 Enterococ	ADY59723 Enterococ	ADY59722 Enterococ	ADY59721 Enterococ	ADY59720 Enterococ	ADY59719 Enterococ	ADY59718 Enterococ	ADY59717 Enterococ	ADY59716 Enterococ	ADY59715 Enterococ	ADY59714 Enterococ	ADY59713 Enterococ	ADY59712 Enterococ	ADY59711 Enterococ	ADY59710 Enterococ	ADY59709 Enterococ	ADY59708 Enterococ	ADY59707 Enterococ	ADY59706 Enterococ	ADY59705 Enterococ	ADY59704 Enterococ	ADY59703 Enterococ	ADY59702 Enterococ	ADY59701 Enterococ	ADY59700 Enterococ	ADY59699 Enterococ	ADY59698 Enterococ	ADY59697 Enterococ	ADY59696 Enterococ	ADY59695 Enterococ	ADY59694 Enterococ	ADY59693 Enterococ	ADY59692 Enterococ	ADY59691 Enterococ	ADY59690 Enterococ	ADY59689 Enterococ	ADY59688 Enterococ	ADY59687 Enterococ	ADY59686 Enterococ	ADY59685 Enterococ	ADY59684 Enterococ	ADY59683 Enterococ	ADY59682 Enterococ	ADY59681 Enterococ	ADY59680 Enterococ	ADY59679 Enterococ	ADY59678 Enterococ	ADY59677 Enterococ	ADY59676 Enterococ	ADY59675 Enterococ	ADY59674 Enterococ	ADY59673 Enterococ	ADY59672 Enterococ	ADY59671 Enterococ	ADY59670 Enterococ	ADY59669 Enterococ	ADY59668 Enterococ	ADY59667 Enterococ	ADY59666 Enterococ	ADY59665 Enterococ	ADY59664 Enterococ	ADY59663 Enterococ	ADY59662 Enterococ	ADY59661 Enterococ	ADY59660 Enterococ	ADY59659 Enterococ	ADY59658 Enterococ	ADY59657 Enterococ	ADY59656 Enterococ	ADY59655 Enterococ	ADY59654 Enterococ	ADY59653 Enterococ	ADY59652 Enterococ	ADY59651 Enterococ	ADY59650 Enterococ	ADY59649 Enterococ	ADY59648 Enterococ	ADY59647 Enterococ	ADY59646 Enterococ	ADY59645 Enterococ	ADY59644 Enterococ	ADY59643 Enterococ	ADY59642 Enterococ	ADY59641 Enterococ	ADY59640 Enterococ	ADY59639 Enterococ	ADY59638 Enterococ	ADY59637 Enterococ	ADY59636 Enterococ	ADY59635 Enterococ	ADY59634 Enterococ	ADY59633 Enterococ	ADY59632 Enterococ	ADY59631 Enterococ	ADY59630 Enterococ	ADY59629 Enterococ	ADY59628 Enterococ	ADY59627 Enterococ	ADY59626 Enterococ	ADY59625 Enterococ	ADY59624 Enterococ	ADY59623 Enterococ	ADY59622 Enterococ	ADY59621 Enterococ	ADY59620 Enterococ	ADY59619 Enterococ	ADY59618 Enterococ	ADY59617 Enterococ	ADY59616 Enterococ	ADY59615 Enterococ	ADY59614 Enterococ	ADY59613 Enterococ	ADY59612 Enterococ	ADY59611 Enterococ	ADY59610 Enterococ	ADY59609 Enterococ	ADY59608 Enterococ	ADY59607 Enterococ	ADY59606 Enterococ	ADY59605 Enterococ	ADY59604 Enterococ	ADY59603 Enterococ	ADY59602 Enterococ	ADY59601 Enterococ	ADY59600 Enterococ	ADY59599 Enterococ	ADY59598 Enterococ	ADY59597 Enterococ	ADY59596 Enterococ	ADY59595 Enterococ	ADY59594 Enterococ	ADY59593 Enterococ	ADY59592 Enterococ	ADY59591 Enterococ	ADY59590 Enterococ	ADY59589 Enterococ	ADY59588 Enterococ	ADY59587 Enterococ	ADY59586 Enterococ	ADY59585 Enterococ	ADY59584 Enterococ	ADY59583 Enterococ	ADY59582 Enterococ	ADY59581 Enterococ	ADY59580 Enterococ	ADY59579 Enterococ	ADY59578 Enterococ	ADY59577 Enterococ	ADY59576 Enterococ	ADY59575 Enterococ	ADY59574 Enterococ	ADY59573 Enterococ	ADY59572 Enterococ	ADY59571 Enterococ	ADY59570 Enterococ	ADY59569 Enterococ	ADY59568 Enterococ	ADY59567 Enterococ	ADY59566 Enterococ	ADY59565 Enterococ	ADY59564 Enterococ	ADY59563 Enterococ	ADY59562 Enterococ	ADY59561 Enterococ	ADY59560 Enterococ	ADY59559 Enterococ	ADY59558 Enterococ	ADY59557 Enterococ	ADY59556 Enterococ	ADY59555 Enterococ	ADY59554 Enterococ	ADY59553 Enterococ	ADY59552 Enterococ	ADY59551 Enterococ	ADY59550 Enterococ	ADY59549 Enterococ	ADY59548 Enterococ	ADY59547 Enterococ	ADY59546 Enterococ	ADY59545 Enterococ	ADY59544 Enterococ	ADY59543 Enterococ	ADY59542 Enterococ	ADY59541 Enterococ	ADY59540 Enterococ	ADY59539 Enterococ	ADY59538 Enterococ	ADY59537 Enterococ	ADY59536 Enterococ	ADY59535 Enterococ	ADY59534 Enterococ	ADY59533 Enterococ	ADY59532 Enterococ	ADY59531 Enterococ	ADY59530 Enterococ	ADY59529 Enterococ	ADY59528 Enterococ	ADY59527 Enterococ	ADY59526 Enterococ	ADY59525 Enterococ	ADY59524 Enterococ	ADY59523 Enterococ	ADY59522 Enterococ	ADY59521 Enterococ	ADY59520 Enterococ	ADY59519 Enterococ	ADY59518 Enterococ	ADY59517 Enterococ	ADY59516 Enterococ	ADY59515 Enterococ	ADY59514 Enterococ	ADY59513 Enterococ	ADY59512 Enterococ	ADY59511 Enterococ	ADY59510 Enterococ	ADY59509 Enterococ	ADY59508 Enterococ	ADY59507 Enterococ	ADY59506 Enterococ	ADY59505 Enterococ	ADY59504 Enterococ	ADY59503 Enterococ	ADY59502 Enterococ	ADY59501 Enterococ	ADY59500 Enterococ	ADY59499 Enterococ	ADY59498 Enterococ	ADY59497 Enterococ	ADY59496 Enterococ	ADY59495 Enterococ	ADY59494 Enterococ	ADY59493 Enterococ	ADY59492 Enterococ	ADY59491 Enterococ	ADY59490 Enterococ	ADY59489 Enterococ	ADY59488 Enterococ	ADY59487 Enterococ	ADY59486 Enterococ	ADY59485 Enterococ	ADY59484 Enterococ	ADY59483 Enterococ	ADY59482 Enterococ	ADY59481 Enterococ	ADY59480 Enterococ	ADY59479 Enterococ	ADY59478 Enterococ	ADY59477 Enterococ	ADY59476 Enterococ	ADY59475 Enterococ	ADY59474 Enterococ	ADY59473 Enterococ	ADY59472 Enterococ	ADY59471 Enterococ	ADY59470 Enterococ	ADY59469 Enterococ	ADY59468 Enterococ	ADY59467 Enterococ	ADY59466 Enterococ	ADY59465 Enterococ	ADY59464 Enterococ	ADY59463 Enterococ	ADY59462 Enterococ	ADY59461 Enterococ	ADY59460 Enterococ	ADY59459 Enterococ	ADY59458 Enterococ	ADY59457 Enterococ	ADY59456 Enterococ	ADY59455 Enterococ	ADY59454 Enterococ	ADY59453 Enterococ	ADY59452 Enterococ	ADY59451 Enterococ	ADY59450 Enterococ	ADY59449 Enterococ	ADY59448 Enterococ	ADY59447 Enterococ	ADY59446 Enterococ	ADY59445 Enterococ	ADY59444 Enterococ	ADY59443 Enterococ	ADY59442 Enterococ	ADY59441 Enterococ	ADY59440 Enterococ	ADY59439 Enterococ	ADY59438 Enterococ	ADY59437 Enterococ	ADY59436 Enterococ	ADY59435 Enterococ	ADY59434 Enterococ	ADY59433 Enterococ	ADY59432 Enterococ	ADY59431 Enterococ	ADY59430 Enterococ	ADY59429 Enterococ	ADY59428 Enterococ	ADY59427 Enterococ	ADY59426 Enterococ	ADY59425 Enterococ	ADY59424 Enterococ	ADY59423 Enterococ	ADY59422 Enterococ	ADY59421 Enterococ	ADY59420 Enterococ	ADY59419 Enterococ	ADY59418 Enterococ	ADY59417 Enterococ	ADY59416 Enterococ	ADY59415 Enterococ	ADY59414 Enterococ	ADY59413 Enterococ	ADY59412 Enterococ	ADY59411 Enterococ	ADY59410 Enterococ	ADY59409 Enterococ	ADY59408 Enterococ	ADY59407 Enterococ	ADY59406 Enterococ	ADY59405 Enterococ	ADY59404 Enterococ	ADY59403 Enterococ	ADY59402 Enterococ	ADY59401 Enterococ	ADY59400 Enterococ	ADY59399 Enterococ	ADY59398 Enterococ	ADY59397 Enterococ	ADY59396 Enterococ	ADY59395 Enterococ	ADY59394 Enterococ	ADY59393 Enterococ	ADY59392 Enterococ	ADY59391 Enterococ	ADY59390 Enterococ	ADY59389 Enterococ	ADY59388 Enterococ	ADY59387 Enterococ	ADY59386 Enterococ	ADY59385 Enterococ	ADY59384 Enterococ	ADY59383 Enterococ	ADY59382 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Enterococ	ADY59329 Enterococ	ADY59328 Enterococ	ADY59327 Enterococ	ADY59326 Enterococ	ADY59325 Enterococ	ADY59324 Enterococ	ADY59323 Enterococ	ADY59322 Enterococ	ADY59321 Enterococ	ADY59320 Enterococ	ADY59319 Enterococ	ADY59318 Enterococ	ADY59317 Enterococ	ADY59316 Enterococ	ADY59315 Enterococ	ADY59314 Enterococ	ADY59313 Enterococ	ADY59312 Enterococ	ADY59311 Enterococ	ADY59310 Enterococ	ADY59309 Enterococ	ADY59308 Enterococ	ADY59307 Enterococ	ADY59306 Enterococ	ADY59305 Enterococ	ADY59304 Enterococ	ADY59303 Enterococ	ADY59302 Enterococ	ADY59301 Enterococ	ADY59300 Enterococ	ADY59299 Enterococ	ADY59298 Enterococ	ADY59297 Enterococ	ADY59296 Enterococ	ADY59295 Enterococ	ADY59294 Enterococ	ADY59293 Enterococ	ADY59292 Enterococ	ADY59291 Enterococ	ADY59290 Enterococ	ADY59289 Enterococ	ADY59288 Enterococ	ADY59287 Enterococ	ADY59286 Enterococ	ADY59285 Enterococ	ADY59284 Enterococ	ADY59283 Enterococ	ADY59282 Enterococ	ADY59281 Enterococ	ADY59280 Enterococ	ADY59279 Enterococ	ADY59278 Enterococ	ADY59277 Enterococ	ADY59276 Enterococ	ADY59275 Enterococ	ADY59274 Enterococ	ADY59273 Enterococ	ADY59272 Enterococ	ADY59271 Enterococ	ADY59270 Enterococ	ADY59269 Enterococ	ADY59268 Enterococ	ADY59267 Enterococ	ADY59266 Enterococ	ADY59265 Enterococ	ADY59264 Enterococ	ADY59263 Enterococ	ADY59262 Enterococ	ADY59261 Enterococ	ADY59260 Enterococ	ADY59259 Enterococ	ADY59258 Enterococ	ADY59257 Enterococ	ADY59256 Enterococ	ADY59255 Enterococ	ADY59254 Enterococ	ADY59253 Enterococ	ADY59252 Enterococ	ADY59251 Enterococ	ADY59250 Enterococ	ADY59249 Enterococ	ADY59248 Enterococ	ADY59247 Enterococ	ADY59246 Enterococ	ADY59245 Enterococ	ADY59244 Enterococ	ADY59243 Enterococ	ADY59242 Enterococ	ADY59241 Enterococ	ADY59240 Enterococ	ADY59239 Enterococ	ADY59238 Enterococ	ADY59237 Enterococ	ADY59236 Enterococ	ADY59235 Enterococ	ADY59234 Enterococ	ADY59233 Enterococ	ADY59232 Enterococ	ADY59231 Enterococ	ADY59230 Enterococ	ADY59229 Enterococ	ADY59228 Enterococ	ADY59227 Enterococ	ADY59226 Enterococ	ADY59225 Enterococ	ADY59224 Enterococ	ADY59223 Enterococ	ADY59222 Enterococ	ADY59221 Enterococ	ADY59220 Enterococ	ADY59219 Enterococ	ADY59218 Enterococ	ADY59217 Enterococ	ADY59216 Enterococ	ADY59215 Enterococ	ADY59214 Enterococ	ADY59213 Enterococ	ADY59212 Enterococ	ADY59211 Enterococ	ADY59210 Enterococ	ADY59209 Enterococ	ADY59208 Enterococ	ADY59207 Enterococ	ADY59206 Enterococ	ADY59205 Enterococ	ADY59204 Enterococ	ADY59203 Enterococ	ADY59202 Enterococ	ADY59201 Enterococ	ADY59200 Enterococ	ADY59199 Enterococ	ADY59198 Enterococ	ADY59197 Enterococ	ADY59196 Enterococ	ADY59195 Enterococ	ADY59194 Enterococ	ADY59193 Enterococ	ADY59192 Enterococ	ADY59191 Enterococ	ADY59190 Enterococ	ADY59189 Enterococ	ADY59188 Enterococ	ADY59187 Enterococ	ADY59186 Enterococ	ADY59185 Enterococ	ADY59184 Enterococ	ADY59183 Enterococ	ADY59182 Enterococ	ADY59181 Enterococ	ADY59180 Enterococ	ADY59179 Enterococ	ADY59178 Enterococ	ADY59177 Enterococ	ADY59176 Enterococ	ADY59175 Enterococ	ADY59174 Enterococ	ADY59173 Enterococ	ADY59172 Enterococ	ADY59171 Enterococ	ADY59170 Enterococ	ADY59169 Enterococ	ADY59168 Enterococ	ADY59167 Enterococ	ADY59166 Enterococ	ADY59165 Enterococ	ADY59164 Enterococ	ADY59163 Enterococ	ADY59162 Enterococ	ADY59161 Enterococ	ADY59160 Enterococ	ADY59159 Enterococ	ADY59158 Enterococ	ADY59157 Enterococ	ADY59156 Enterococ	ADY59155 Enterococ	ADY59154 Enterococ	ADY59153 Enterococ	ADY59152 Enterococ	ADY59151 Enterococ	ADY59150 Enterococ	ADY59149 Enterococ	ADY59148 Enterococ	ADY59147 Enterococ	ADY59146 Enterococ	ADY59145 Enterococ	ADY59144 Enterococ	ADY59143 Enterococ	ADY59142 Enterococ	ADY59141 Enterococ	ADY59140 Enterococ	ADY59139 Enterococ	ADY59138 Enterococ	ADY59137 Enterococ	ADY59136 Enterococ	ADY59135 Enterococ	ADY59134 Enterococ	ADY59133 Enterococ	ADY59132 Enterococ	ADY59131 Enterococ	ADY59130 Enter
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93	17.6	65.2	1026	4	AA553038	AA553038 Enterococ
94	17.6	65.2	4948	2	AA742134	AA742134 ITC-1 gen
95	17.6	65.2	39982	8	AA448290	AA448290 Human enz
96	17.6	65.2	66685	4	AA507380	AA507380 Human gen
97	17.6	65.2	66686	6	AA507380	AA507380 Human gen
98	17.4	64.4	318	10	ACF68191	ACF68191 Photorhab
99	17.4	64.4	486	3	AA54587	AA54587 Human col
100	17.4	64.4	747	4	AA54529	AA54529 Neisseria
101	17.4	64.4	754	12	AD062241	AD062241 Transcrip
102	17.4	64.4	1053	11	ABD12723	ABD12723 Pseudom
103	17.4	64.4	1200	11	ADK06068	ADK06068 Plant ful
104	17.4	64.4	1262	12	AD063288	AD063288 Transcrip
105	17.4	64.4	1310	12	AD062242	AD062242 Transcrip
106	17.4	64.4	1353	13	ADK53082	ADK53082 Plant ful
107	17.4	64.4	1512	11	ABD12707	ABD12707 Pseudom
108	17.4	64.4	1865	12	AD062245	AD062245 Transcrip
109	17.4	64.4	2334	11	ABD12689	ABD12689 Pseudom
110	17.4	64.4	3274	2	AAV17622	AAV17622 Plasm sat
111	17.4	64.4	4081	2	AAV06585	AAV06585 Arabidops
112	17.4	64.4	23070	9	ADA02507	ADA02507 Mouse Wnt
113	17.4	64.4	23070	10	AD872245	AD872245 Mouse Wnt
114	17.4	64.4	23070	10	AD872245	AD872245 Mouse Wnt
115	17.4	64.4	23982	14	AD212503	AD212503 Murine ca
116	17.4	64.4	73882	13	AD573531	AD573531 tcp gene
117	17.4	64.4	110000	10	ACF67367_09	ACF67367_09 Cont
118	17.4	64.4	110000	10	ACF65384_3	ACF65384_3 Cont
119	17.4	64.4	11836	13	ABD33102	ABD33102 Murine ca
120	17.4	64.4	256525	11	ACM44148	ACM44148 Mouse gen

ALIGNMENTS

RESULT 1
AD59929 standard; DNA; 27 BP.

AD59929;
17-MAR-2005.
12-SEP-2003; 2003US-00661094.
12-SEP-2003; 2003US-00661094.
(DODG/) DODGSON K J.
Dodgson KJ;
WPI; 2005-222218/23.

Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA- and/or vanB-specific oligonucleotide probes or primers.

Claim 34; SEQ ID NO 3; 33pp; English.

The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an

oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the vanA gene, or its complement or portion, or an oligonucleotide comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 425-446 of the vanB gene, or its complement or portion, where the oligonucleotide hybridizes under stringent hybridization conditions to vanA or vanB DNA; and (2) a kit comprising one or more oligonucleotide(s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products requiring microbiological control. The present sequence represents a probe for Enterococcus faecium vanA, which is used in an example, from the present invention.

Sequence 27 BP; 3 A; 8 G; 6 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 14; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGATCCGTTTGTGTTAAAGCCGCGCC 27
Db 1 CCGATCCGTTTGTGTTAAAGCCGCGCC 27

RESULT 2
AAH02300 standard; DNA; 1032 BP.

AAH02300;
24-JUL-2001 (first entry)

Enterococcus faecium nucleotide sequence SEQ ID NO:2293.

Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitic; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine; primer; ds.

Enterococcus faecium.

WO200123604-A2.
05-APR-2001.
28-SEP-2000; 2000NO-CA001150.
28-SEP-1999; 99CA-02283458.
19-MAY-2000; 2000CA-02307010.
(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
Bergerson MG, Boissinot M, Huletsky A, Menard C, Ouellette M; Picard FJ, Roy PH;
WPI; 2001-245006/25.

Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitic species in a test sample.

Disclosure; Page 1578; 1580pp; English.

The present invention describes a method for generating a repository of nucleic acids of tuf, tps, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic

acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (1) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene, hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (1) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Baccherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

XX Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCGGCGC 27
DB 494 CCTATCCTGTTTGTAAAGCGGCGC 520

RESULT 3

AAAF6039
ID AAFF6039 standard; DNA; 1032 BP.

AC AAFF6039;

DT 22-MAY-2001 (first entry)

DE Enterococcus faecium vanA gene, SEQ ID NO:21.

XX Vancomycin resistance reduction; antisense expression inhibition;

KM competitive inducer sequestration; vanH promoter; vanH gene product;

KM Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium;

KM antibiotic susceptibility; ex vivo eradication; in vivo eradication;

XX glycopeptide resistance; VanA gene cluster; ds.

OS Enterococcus faecium.

PN WO200112803-A2.

PD 22-FEB-2001.

PF 11-AUG-2000; 2000WO-US022086.

PR 17-AUG-1999; 99US-0149313P.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Inouye RT, Torres-Viera C, Moellerling R, Gold H, Eliopoulos GM;

XX WPI; 2001-211216/21.

XX Reducing vancomycin-resistance in vancomycin-resistant organism by

XX introducing a antisense vancomycin-resistance molecule to inhibit

XX vancomycin-resistance gene expression, or by enhancing vanH promoter

XX expression.

XX Example; Page 52; 59pp; English.

CC The invention relates to methods of reducing vancomycin resistance in a
CC vancomycin-resistant organism. One method involves introducing a
CC vancomycin resistance gene antisense nucleic acid into the organism;
CC antisense oligonucleotides complementary to AAFF6033-AAFF6031 are
CC particularly preferred for this purpose. The second method involves
CC providing additional vanH promoter sequences which are not operatively
CC coupled to a vancomycin resistance gene, so that the phosphorylated vanH
CC gene product (which induces vanH promoter activity) is competitively
CC sequestered. Both methods are able to restore antibiotic susceptibility
CC in glycopeptide resistant enterococci. The methods of the invention are
CC useful for reducing vancomycin resistance in a vancomycin resistant
CC organism, particularly Enterococcus faecium and Enterococcus faecalis,
CC but also in other Gram-positive bacteria such as Staphylococcus sp. and
CC Streptococcus sp., to which Enterococcus faecium and Enterococcus
CC faecalis have the potential to transfer resistance determinants. The
CC antisense molecules are useful in the treatment of infection and
CC colonisation by vancomycin resistant enterococci and other clinically
CC significant pathogens, and may be used for the ex vivo eradication of
CC vancomycin-resistant enterococci from frequently colonised settings, such
CC as intensive care units, haemodialysis units, and chronic care facilities
CC ; for the in vivo clearance of vancomycin-resistant enterococci from
CC colonised gastrointestinal or genitourinary tracts of animals, including
CC humans; and in primary or adjuvant therapy for vancomycin-resistant
CC enterococcal infections. The gene based strategy targets key vancomycin
CC resistance determinants and results in restoration of vancomycin
CC susceptibility in previously glycopeptide-resistant enterococci.
CC Sequences AAFF6036-AAFF6042 represent genes of the Enterococcus faecium
CC VanA gene cluster

XX Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCGGCGC 27
DB 494 CCTATCCTGTTTGTAAAGCGGCGC 520

RESULT 4

AAH01064
ID AAH01064 standard; DNA; 1218 BP.

AC AAH01064;

DT 24-JUL-2001 (first entry)

DE Enterococcus gallinarum nucleotide sequence SEQ ID NO:1055.

XX Species specific; genus specific; family specific; probe; detection;

KM identification; algal; archaeal; bacterial; fungal; parasitological;

KM microorganism; diagnosis; translation elongation factor Tu; toxin;

KM translation elongation factor G; RecA recombinase; resistance;

KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;

XX primer; ds.

XX Enterococcus gallinarum.

XX WO200123604-A2.

PN 05-APR-2001.

PF 28-SEP-2000; 2000WO-CA001150.

PR 28-SEP-1999; 99CA-02283458.

XX 19-MAY-2000; 2000CA-02307010.

XX (INFB-) INFECTIO DIAGNOSTIC (IDI) INC.

XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

XX Picard FJ, Roy PH;

DR WPI, 2001-245006/25.

XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PI bacterial, fungal and parasitological species in a test sample.

PS Claim 27, Page 1001-1002; 1580pp; English.

XX The present invention describes a method for generating a repository of
CC nucleic acids of ruf, fuf, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

SQ Sequence 1218 BP; 364 A; 226 C; 311 G; 317 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1218;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTTAAGCGCGC 27

Db 568 CCTATCCTGTTTGTTAAGCGCGC 594

RESULT 5

AAH01063 ID AAH01063 standard; DNA; 1232 BP.

XX AAH01063;

DT 24-JUL-2001 (first entry)

DE Enterococcus faecalis nucleotide sequence SEQ ID NO:1054.

XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitological;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.

XX Enterococcus faecalis.

XX WO200123604-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-CA001150.

XX 28-SEP-1999; 99CA-02283458.

XX 19-MAY-2000; 2000CA-02307010.

PA (INFR-) INFECTIO DIAGNOSTIC (IDI) INC.

PI Bergeron MG, Bolesnot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;

XX WPI, 2001-245006/25.

PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PI bacterial, fungal and parasitological species in a test sample.

PS Claim 27, Page 1001; 1580pp; English.

XX The present invention describes a method for generating a repository of
CC nucleic acids of ruf, fuf, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

SQ Sequence 1232 BP; 367 A; 228 C; 313 G; 323 T; 0 U; 1 Other;

Query Match 100.0%; Score 27; DB 4; Length 1232;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTTAAGCGCGC 27

Db 578 CCTATCCTGTTTGTTAAGCGCGC 604

RESULT 6

AAH01061 ID AAH01061 standard; DNA; 1237 BP.

XX AAH01061;

DT 24-JUL-2001 (first entry)

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1052.

XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitological;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.

XX Enterococcus faecium.

XX WO200123604-A2.

XX 05-APR-2001.

PF 28-SEP-2000; 2000MO-CA001150.
XX
XX 28-SEP-1999; 99CA-02283458.
FR 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
XX Bergerson MG, Bolssinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX WPI; 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitological species in a test sample.
XX
XX Claim 27; Page 999; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpd and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
XX Sequence 1237 BP; 366 A; 235 C; 314 G; 322 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 27; DB 4; Length 1237;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCTATCCTGTTTCTTAAGCGGCGC 27
DB 590 CCTATCCTGTTTCTTAAGCGGCGC 616
RESULT 7
AAH01058
ID AAH01058 standard; DNA; 1241 BP.
XX
XX AAH01058;
XX
XX 24-JUL-2001 (first entry)
XX
XX Enterococcus faecium nucleotide sequence SEQ ID NO:1049;
XX
XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitological;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; ds.
XX
XX Enterococcus faecium.
OS

XX
XX WO200123604-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 28-SEP-2000; 2000MO-CA001150.
PF
XX
XX 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
XX Bergerson MG, Bolssinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX WPI; 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitological species in a test sample.
XX
XX Claim 27; Page 997; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpd and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
XX Sequence 1241 BP; 371 A; 228 C; 317 G; 325 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 27; DB 4; Length 1241;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCTATCCTGTTTCTTAAGCGGCGC 27
DB 561 CCTATCCTGTTTCTTAAGCGGCGC 587
RESULT 8
AAH01059
ID AAH01059 standard; DNA; 1249 BP.
XX
XX AAH01059;
XX
XX 24-JUL-2001 (first entry)
XX
XX Enterococcus gallinarum nucleotide sequence SEQ ID NO:1050.
XX
XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitological;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX

KM translation elongation factor G; RecA recombinase; resistance;
 KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KM primer; ds.
 XX
 OS Enterococcus gallinarum.
 XX
 PN MO200123604-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000MO-CA001150.
 XX
 PR 28-SEP-1999; 99CA-02283458.
 PR 19-MAY-2000; 2000CA-02307010.
 XX
 PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 XX
 PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX
 DR WPI; 2001-245006/25.
 XX
 PT Nucleic acid sequences are used to generate universal probes and primers
 PT which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitological species in a test sample.
 PS Claim 27; Page 998; 1580p; English.
 XX
 CC The present invention describes a method for generating a repository of
 CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitological
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and identification of an algal, archaeal, bacterial, fungal and
 CC parasitological species, genus, family and group. A nucleic acid (I) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
 CC at least one antimicrobial agent resistance gene or at least one toxin
 CC gene. hexA nucleic acids are used for the specific and ubiquitous
 CC detection and for identification of Streptococcus pneumoniae. (I) can be
 CC used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
 CC Corynebacterium sp., Enterobacteriaceae group, Baccharichia coli,
 CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
 CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 CC results than substrate specificity tests as results can be determined in
 CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1249 BP; 373 A; 235 C; 316 G; 325 T; 0 U; 0 Other;
 XX
 QY Query Match 100.0%; Score 27; DB 4; Length 1249;
 Db Best Local Similarity 100.0%; Pred. NO. 0.031;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CCGATCCGTTTGTGTTAAGCCGCGC 27
 590 CCGATCCGTTTGTGTTAAGCCGCGC 616
 RESULT 9
 AAH01062
 ID AAH01062 standard; DNA; 1263 BP.
 XX
 AC AAH01062;
 XX
 DT 24-JUL-2001 (first entry)
 XX

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1053.
 XX
 XX Species specific; genus specific; family specific; probe; detection;
 KM identification; algal; archaeal; bacterial; fungal; parasitological;
 KM microorganisms; diagnosis; translation elongation factor Tuf; toxin;
 KM translation elongation factor G; RecA recombinase; resistance;
 KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KM primer; ds.
 XX
 OS Enterococcus faecium.
 XX
 PN MO200123604-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000MO-CA001150.
 XX
 PR 28-SEP-1999; 99CA-02283458.
 PR 19-MAY-2000; 2000CA-02307010.
 XX
 PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 XX
 PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX
 DR WPI; 2001-245006/25.
 XX
 PT Nucleic acid sequences are used to generate universal probes and primers
 PT which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitological species in a test sample.
 PS Claim 27; Page 1000; 1580p; English.
 XX
 CC The present invention describes a method for generating a repository of
 CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitological
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and identification of an algal, archaeal, bacterial, fungal and
 CC parasitological species, genus, family and group. A nucleic acid (I) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
 CC at least one antimicrobial agent resistance gene or at least one toxin
 CC gene. hexA nucleic acids are used for the specific and ubiquitous
 CC detection and for identification of Streptococcus pneumoniae. (I) can be
 CC used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
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 CC Corynebacterium sp., Enterobacteriaceae group, Baccharichia coli,
 CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
 CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 CC results than substrate specificity tests as results can be determined in
 CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1263 BP; 378 A; 234 C; 321 G; 330 T; 0 U; 0 Other;
 XX
 QY Query Match 100.0%; Score 27; DB 4; Length 1263;
 Db Best Local Similarity 100.0%; Pred. NO. 0.031;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CCGATCCGTTTGTGTTAAGCCGCGC 27
 582 CCGATCCGTTTGTGTTAAGCCGCGC 608
 RESULT 10
 AAH01065
 ID AAH01065 standard; DNA; 1265 BP.
 XX

XX AAH01065;
 AC
 XX
 XX 24-JUL-2001 (first entry)
 DT
 XX Enterococcus faecium nucleotide sequence SEQ ID NO:1056.
 DE
 XX Species specific; genus specific; family specific; probe; detection;
 KM identification; algal; archaeal; bacterial; fungal; parasitical;
 KM microorganism; diagnosis; translation elongation factor Tu; toxin;
 KM translation elongation factor G; RecA recombinase; resistance;
 KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KM primer; ds.
 XX
 XX Enterococcus faecium.
 OS
 XX MO200123604-A2.
 PN
 XX 05-APR-2001.
 PD
 XX 28-SEP-2000; 2000MO-CA001150.
 PF
 XX 28-SEP-1999; 99CA-02283458.
 PR
 XX 19-MAY-2000; 2000CA-02307010.
 XX
 PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX WPI; 2001-245006/25.
 DR
 XX Nucleic acid sequences are used to generate universal probes and primers
 PT which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitical species in a test sample.
 PS
 XX Claim 27; Page 1002; 1580pp; English.
 CC The present invention describes a method for generating a repository of
 CC nucleic acids of tuf, fus, apd and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitical
 CC species with a combination of defined primer pairs. The method can be
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 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
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 CC parasitical species, genus, family and group. A nucleic acid (I) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
 CC at least one antimicrobial agent resistance gene or at least one toxin
 CC gene. hexA nucleic acids are used for the specific and ubiquitous
 CC detection and for identification of Streptococcus pneumoniae. (I) can be
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 CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
 CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
 CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 CC results than substrate specificity tests as results can be determined in
 CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention.
 CC
 XX Sequence 1265 BP; 379 A; 237 C; 320 G; 329 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 27; DB 4; Length 1265;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 ID AAH01066 standard; DNA; 1269 BP.
 XX
 XX AAH01066;
 AC
 XX 24-JUL-2001 (first entry)
 DT
 XX Enterococcus faecium nucleotide sequence SEQ ID NO:1057.
 DE
 XX Species specific; genus specific; family specific; probe; detection;
 KM identification; algal; archaeal; bacterial; fungal; parasitical;
 KM microorganism; diagnosis; translation elongation factor Tu; toxin;
 KM translation elongation factor G; RecA recombinase; resistance;
 KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KM primer; ds.
 XX
 XX Enterococcus faecium.
 OS
 XX MO200123604-A2.
 PN
 XX 05-APR-2001.
 PD
 XX 28-SEP-2000; 2000MO-CA001150.
 PF
 XX 28-SEP-1999; 99CA-02283458.
 PR
 XX 19-MAY-2000; 2000CA-02307010.
 XX
 PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX WPI; 2001-245006/25.
 DR
 XX Nucleic acid sequences are used to generate universal probes and primers
 PT which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitical species in a test sample.
 PS
 XX Claim 27; Page 1003; 1580pp; English.
 CC The present invention describes a method for generating a repository of
 CC nucleic acids of tuf, fus, apd and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitical
 CC species with a combination of defined primer pairs. The method can be
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 CC parasitical species, genus, family and group. A nucleic acid (I) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
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 CC results than substrate specificity tests as results can be determined in
 CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention
 CC
 XX Sequence 1269 BP; 380 A; 238 C; 321 G; 330 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 27; DB 4; Length 1269;
 Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTATCCTGTTTGTAAAGCCGCGC 27
Db 590 CCTATCCTGTTTGTAAAGCCGCGC 616

RESULT 12
AAH01060
ID AAH01060 standard; DNA; 1272 BP.
XX
XX AAH01060;
XX
XX 24-JUL-2001 (first entry)
XX
XX

Enterococcus faecium nucleotide sequence SEQ ID NO:1051.

Species specific; genus specific; family specific; probe; detection;
identification; algal; archaeal; bacterial; fungal; parasitica;
microorganism; diagnosis; translation elongation factor Tu; toxin;
translational elongation factor G; RecA recombinase; resistance;
catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
primer; ds.

Enterococcus faecium.
MO200123604-A2.

05-APR-2001.

28-SEP-2000; 2000MO-CA001150.

28-SEP-1999; 99CA-02283458.

19-MAY-2000; 2000CA-02307010.

(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

Bergeon MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
Picard FJ, Roy PH;
XX
XX WPI; 2001-245006/25.

Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
XX bacterial, fungal and parasitica species in a test sample.

Claim 27; Page 998-999; 1580pp; English.

XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitica
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitica species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
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CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

XX SQ Sequence 1272 BP; 379 A; 232 C; 325 G; 336 T; 0 U; 0 Other;
Query Match 100.0%; Score 27; DB 4; Length 1272;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTAAAGCCGCGC 27
Db 570 CCTATCCTGTTTGTAAAGCCGCGC 596

RESULT 13
AAH01148
ID AAH01148 standard; DNA; 1768 BP.
XX
XX AAH01148;
XX
XX 24-JUL-2001 (first entry)
XX
XX

Enterococcus faecium nucleotide sequence SEQ ID NO:1139.

Species specific; genus specific; family specific; probe; detection;
identification; algal; archaeal; bacterial; fungal; parasitica;
microorganism; diagnosis; translation elongation factor Tu; toxin;
translational elongation factor G; RecA recombinase; resistance;
catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
primer; ds.

Enterococcus faecium.
MO200123604-A2.

05-APR-2001.

28-SEP-2000; 2000MO-CA001150.

28-SEP-1999; 99CA-02283458.

19-MAY-2000; 2000CA-02307010.

(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

Bergeon MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
Picard FJ, Roy PH;
XX
XX WPI; 2001-245006/25.

Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
XX bacterial, fungal and parasitica species in a test sample.

Disclosure; Page 1033-1034; 1580pp; English.

XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitica
CC species with a combination of defined primer pairs. The method can be
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CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitica species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria

gonorrhoeae and *Staphylococcus* sp. . Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH0010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention

Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTGTTAGCCGCGC 27
870 CCTATCCTGTTTGTGTTAGCCGCGC 896

RESULT 14

ID ADO47257 standard; DNA; 1768 BP.

ADO47257;

15-JUL-2004 (first entry)

E. faecium vancomycin resistance gene, vanA.

Vancomycin resistant enterococcus; vancomycin resistance gene; vanA;

gene; de; hospital acquired infection; VRB;

fluorescence resonance energy transfer; FRRET.

Enterococcus faecium.

US2004058336-A1.

25-MAR-2004.

25-SRP-2002; 2002US-00254260.

25-SRP-2002; 2002US-00254260.

(COCK/) COCKERILL F R.

(SLOAN/) SLOAN L M.

Cockerill FR, Sloan LM;

WPI; 2004-268785/25.

Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase chain reaction.

disclosure; SEQ ID NO 10; 23pp; English.

The invention relates to detecting the presence or absence of vancomycin-resistant enterococci (VRB) in a sample, comprising performing a cycling step by amplifying a sample with pair of vanA or vanB primers and hybridizing the sample with a pair of vanA or vanB probes, labelled with donor and acceptor fluorescent group, respectively, detecting fluorescence resonance energy transfer (FRRET), where the presence of FRRET indicates presence of VRB. Also included is an article of manufacture, comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes and a donor fluorescent group and a corresponding fluorescent group. The method is useful for detecting the presence or absence of vancomycin-resistant enterococci in a biological sample, e.g. stool samples, anal or perirectal swabs, blood and body fluids from an individual. The method replaces standard culture methods and reduces the cost. The method provides rapid vancomycin resistant enterococcus real time PCR assay which is useful for beginning the antimicrobial therapy immediately to treat hospital acquired infection. The present sequence is an enterococcal vanA, vancomycin resistance gene.

Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 12; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTGTTAGCCGCGC 27
870 CCTATCCTGTTTGTGTTAGCCGCGC 896

RESULT 15

ID ADY59927 standard; DNA; 1768 BP.

ADY59927;

02-JUN-2005 (first entry)

Enterococcus faecium vanA DNA sequence SEQ ID NO:1.

DNA detection; antibiotic-resistance; vancomycin; vanA; gene; de.

Enterococcus faecium.

US2005058985-A1.

17-MAR-2005.

12-SRP-2003; 2003US-00661094.

12-SRP-2003; 2003US-00661094.

(DODG/) DODGSON K J.

Dodgson KJ;

WPI; 2005-222218/23.

Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA- and/or vanB-specific oligonucleotide probes or primers.

Example 1; SEQ ID NO 1; 33pp; English.

The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the vanA gene, or its complement or portion, or an oligonucleotide comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonucleotide hybridizes under stringent hybridization conditions to vanA or vanB DNA; and (2) a kit comprising one or more oligonucleotide(s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products requiring microbiological control. The present sequence represents an *Enterococcus faecium* vanA nucleotide sequence from the present invention.

Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 14; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTGTTAGCCGCGC 27

Db 870 CCTATCCTGTTTGTAAAGCCGCCG 896

RESULT 16
AAT28569

ID AAT28569 standard; DNA; 2607 BP.

XX AAT28569;

DT 01-APR-1997 (first entry)

DE Bacterial antibiotic resistance gene, vanM, vanA and vanX, probe.

XX Detection; probe: amplification primer; bacterial pathogen; pneumonia;
KM Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
KM Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
KM Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
KM Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
KM Haemophilus influenzae; Moraxella catarrhalis; septicemia; meningitis;
KM infection; intra-abdominal infection; skin infection;
KM bacterial resistance; beta-lactam antibiotic; ds.

XX Synthetic.

OS MO608582-A2.

PN 21-MAR-1996.

PF 12-SEP-1995; 95WO-CA000528.

PR 12-SEP-1994; 94US-00304732.

XX (BERG/) BERGERON M. G.

PA (OUEL/) OUELLETTE M.

XX (ROYP/) ROY P. H.

PI Bergeron MG, Ouellette M, Roy PH;

XX WPI; 1996-1179953/18.

PT Method for the detection of bacterial species using probes and primers -

PT allows detection and quantification of antibiotic resistant bacteria in

PT patients, the environment and food.

XX Claim 94; Page 145-147; 216pp; English.

XX The sequences given in AAT28560-76 represent fragments derived from
CC bacterial antibiotic resistance genes which were used as probes in the
CC method of the invention for the detection of bacterial species in a
CC sample. The method of the invention comprises using probes and/or
CC amplification primers which are specific, ubiquitous and sensitive for
CC determining the presence and/or amount of nucleic acids from selected
CC bacterial species in any sample, where the bacterial nucleic acid
CC comprises a selected target region hybridisable with the probes or
CC primers. The method comprises contacting the sample with the probes or
CC primers and detecting the presence and/or amount of hybridised primers or
CC amplification products as and indication of the presence and/or amount of
CC the bacterial species. This method may be used to detect commonly
CC encountered bacterial pathogens, e.g. Escherichia coli, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus
CC pneumoniae, Staphylococcus aureus, Staphylococcus epidermidis,
CC Enterococcus faecalis, Staphylococcus saprophyticus, Streptococcus
CC pyogenes, Haemophilus influenzae and Moraxella catarrhalis. These
CC bacterial species are associated with approx. 90% of urinary tract
CC infections and with a high percentage of other severe infections
CC including septicemia, meningitis, pneumonia, intra-abdominal infections,
CC skin infections and other severe respiratory tract infections. The method
CC may also be used to evaluate a bacterial resistance to beta-lactam
CC antibiotics

XX Sequence 2607 BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 2; Length 2607;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCCGCCG 27
DB 1455 CCTATCCTGTTTGTAAAGCCGCCG 1481

RESULT 17

ABA76994

ID ABA76994 standard; DNA; 2607 BP.

XX ABA76994;

DT 28-JAN-2002 (first entry)

DE Antibiotic resistance detection polynucleotide SEQ ID NO 170.

XX Detection; bacterial species; animal; food; environment;

XX antibiotic resistance; ds.

XX Undifferentiated.

OS N2501596-A.

PN 29-JUN-2001.

PF 12-SEP-1995; 95NZ-00501596.

PR 12-SEP-1995; 95NZ-00501596.

XX (IDI-) IDI INFECTIO DIAGNOSTIC INC.

PI Bergeron MG, Ouellette M, Roy PH;

XX WPI; 2001-615034/71.

PT Method for detecting target bacterial species in a sample, comprises

PT detecting the presence or amount of bacterial nucleic acid amplified by a

PT primer derived from bacterial DNA, specific for the target bacterial

PT species.

XX Claim 16; Page 160-162; 168pp; English.

XX The invention relates to detecting target bacterial species suspected to
CC be present in a sample, comprising contacting nucleic acids of target
CC bacterial species with an amplification primer pair derived from a
CC bacterial DNA fragment (ABA76825-ABA76861) specific for the target
CC bacterial species but ubiquitous for different strains, amplifying the
CC nucleic acid and detecting the presence or amount of an amplified
CC sequence as an indication of the presence or amount of the target
CC bacterial species. The invention includes primers and probes (ABA76862-
CC ABA76984) against the target bacterial species, especially E.coli,
CC K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae, S.aureus,
CC M.catarrhalis and/or group A Streptococci producing exotoxin A gene spe
CC A, suspected to be present in a sample which is obtained from human
CC patients, animals, environment or food, and which consists of one or more
CC bacterial colonies. Oligonucleotide probes and primers complementary to
CC the bacterial genes encoding resistance to antibiotics such as bla(tem),
CC bla(rob), bla(shv), aacB, aacC1, aacC3, aacA4, meca, vanA, vanM,
CC vanX, aacA, aacA-hd, vat, yga, mcrA, sul and/or int (ABA76985-ABA77001)
CC are also useful to identify commonly encountered and clinically important
CC resistance genes. The invention provides a rapid method of bacterial
CC identification that can be achieved, which reduces the time currently
CC required for the identification of pathogens in the clinical laboratory

XX Sequence 2607 BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 2607;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCGGCGC 27
DB 1455 CCTATCCTGTTTGTAAAGCGGCGC 1481

RESULT 18

AAH01150
ID AAH01150 standard; DNA; 3946 BP.

AAH01150;

24-JUL-2001 (first entry)

Enterococcus faecium nucleotide sequence. SEQ ID NO:1141.

Species specific; genus specific; family specific; probe; detection;
identification; algal; archaeal; bacterial; fungal; parasitological;
microorganism; diagnosis; translation elongation factor Tu; toxin;
translation elongation factor G; RecA recombinase; resistance;
catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
primer; ds.

Enterococcus faecium.

MO200123604-A2.

05-APR-2001.

28-SBP-2000; 2000MO-CA001150.

28-SBP-1999; 99CA-02283458.

19-MAY-2000; 2000CA-02307010.

(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

Bergeon MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

Picard FJ, Roy PH;

WPI; 2001-245006/25.

Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitological species in a test sample.

Disclosure; Page 1035-1036; 1580pp; English.

The present invention describes a method for generating a repertoire of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitological species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitological species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention

SQ Sequence 3946 BP; 1235 A; 706 C; 936 G; 1069 T; 0 U; 0 Other;
Query Match 100.0%; Score 27; DB 4; Length 3946;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCGGCGC 27

DB 1455 CCTATCCTGTTTGTAAAGCGGCGC 1481

RESULT 19

AAQ25183
ID AAQ25183 standard; DNA; 7227 BP.

AAQ25183;

24-OCT-2003 (revised)

25-MAR-2003 (revised)

20-NOV-1992 (first entry)

E faecium antibiotic resistance genes and flanking sequences.

Glycopeptide antibiotic; Vancomycin; telcoplanin; resistant;

D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;

inverted repeats; vanR; vanS; vanH; vanA; vanX; ss.

Enterococcus faecium; BM4147.

MO9207942-A1.

14-MAY-1992.

29-OCT-1991; 91MO-FR000855.

31-OCT-1990; 90FR-00013579.

(INSP) INST PASTEUR.

Arthur M, Dukta-Malen S, Molinas C, Courvillain P;

WPI; 1992-183677/22.

P-PSDB; AAR24305, AAR24306, AAR24307.

Polypeptides involved in expression of glycopeptide antibiotic resistance

- useful in diagnosing presence of gram-positive enterococcal strains

e.g. Enterococcus faecium and E Gallinarum.

Disclosure; Fig 4; 163pp; French.

This sequence contains the genes vanH, vanA, vanX, vanR and vanS. The

proteins encoded by the latter two genes (i.e. proteins VanR and VanS)

have a regulatory function and control expression of the other three

("protective") proteins. See also AAQ25179-025182. (Updated on 25-MAR-

2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)

(Updated on 24-OCT-2003 to standardise OS field)

Sequence 7227 BP; 2313 A; 1305 C; 1596 G; 2011 T; 0 U; 2 Other;

Query Match 100.0%; Score 27; DB 2; Length 7227;

Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCGGCGC 27

DB 5018 CCTATCCTGTTTGTAAAGCGGCGC 5044

RESULT 20

AAQ25178
ID AAQ25178 standard; DNA; 10851 BP.

AAQ25178;

XX	24-OCT-2003	(revised)
DT	25-MAR-2003	(revised)
DT	20-NOV-1992	(first entry)
XX		
DE	E.faecium antibiotic resistance genes and Tn sequences.	
XX		
KW	Glycopeptide antibiotic; vancomycin; telicoplanin; resistant;	
KM	D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;	
KX	inverted repeats; ss.	
XX		
OS	Enterococcus faecium; BM4147.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	complement(1..318)
FT		/*tag= a
FT		/product= "transposase"
FT		/note= "coded by the (-) strand - see AAQ25179"
FT	repeat_unit	1..38
FT		/*tag= j
FT		/rpt_type= INVERTED
FT		3187..3762
FT		/*tag= b
FT		/product= "resolvase"
FT		3976..4671
FT		/*tag= c
FT		/product= "VanR"
FT		/note= "VanR is a transcription activator"
FT	CDS	4649..5803
FT		/*tag= d
FT		/product= "Vans"
FT		/note= "Vans is a regulatory protein"
FT		6018..6986
FT	CDS	/*tag= e
FT		/product= "VanH"
FT		6979..8010
FT		/*tag= f
FT		/product= "VanA"
FT	CDS	8016..8624
FT		/*tag= g
FT		/product= "VanX"
FT		9052..9963
FT		/*tag= h
FT		/product= "VanY"
FT	CDS	10116..10601
FT		/*tag= i
FT		/product= "VanZ"
FT		complement(10814..10851)
FT	repeat_unit	/*tag= k
FT		/rpt_type= INVERTED
XX		
PN	WO9207942-A1.	
XX		
DD	14-MAY-1992.	
XX		
PP	29-OCT-1991;	91WO-FR000855.
XX		
PR	31-OCT-1990;	90FR-00013579.
XX		
PA	(INSP) INST PASTEUR.	
XX		
PI	Arthur M, Dukta-Malen S, Molinas C, Courvalin P,	
XX		
DR	WPI, 1992-183677/22.	
XX	P-PBDB; AAR24294, AAR24295, AAR24296, AAR24297, AAR24298, AAR24299,	
DR	AAR24300, AAR24301, AAR24302.	
XX		
PT	Polypeptides involved in expression of glycopeptide antibiotic resistance	
PT	- useful in diagnosing presence of Gram-positive enterococcal strains	
PT	e.g. Enterococcus Faecium and E Gallinarum.	
PS	Claim 9, Fig 8, 163pp; French.	
XX		

This is a transposon sequence. The transposon comprises the genes necessary for expression of resistance to glycopeptides in *Enterococcus faecium*. It also contains genes associated with resistance, e.g. involved in regulation of expression of the resistance genes or in the amount of polypeptide produced. See also AAQ25179-Q25183. (Updated on 25-Mar-2003 to correct PN field.) (Updated on 25-Mar-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS field)

SQ Sequence 10851 BP, 3399 A, 1960 C, 2234 G, 3256 T, 0 U, 0 Other;

Query Match 100.0%; Score 27; DB 2; Length 10851;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 27, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

1 CCTATCCGCTTTTGTTAGCGGCGC 27
 |||||
 Db 7472 CCTATCCGTTTGTTAGCGGCGC 7498

RESULT 21
 AAF76019
 ID AAF76019 standard; DNA; 10851 BP.
 XX
 AC AAF76019;
 XX
 DT 22-MAY-2001 (first entry)
 DE E. faecium Vana vancomycin resistance gene cluster, SEQ ID NO:1.
 XX
 KW Vancomycin resistance reduction; antisense expression inhibition;
 KW competitive inducer sequestration; vanH promoter; vanR gene product;
 KW Enterococcus; *Staphylococcus*; *Streptococcus*; Gram-positive bacterium;
 KW antibiotic susceptibility; ex vivo eradication; in vivo eradication;
 KW glycopeptide resistance; Vana gene cluster; de.
 XX
 OS Enterococcus faecium.
 XX
 PN WO200112803-A2.
 PD 22-FEB-2001.
 XX
 PF 11-AUG-2000; 2000WO-US022086.
 XX
 PR 17-AUG-1999; 99US-0149313P.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Inouye RT, Torres-Viera C, Moellering R, Gold H, Ellopoulos GM;
 XX
 DR WPI; 2001-211216/21.
 XX
 PT Reducing vancomycin-resistance in vancomycin-resistant organism by
 PT introducing a antisense vancomycin-resistance molecule to inhibit
 PT vancomycin-resistance gene expression, or by enhancing vanH promoter
 PT expression.
 PT
 PS Claim 24; Page 41-44; 59pp; English.
 XX
 PS The invention relates to methods of reducing vancomycin resistance in a
 CC vancomycin-resistant organism. One method involves introducing a
 CC vancomycin resistance gene antisense nucleic acid into the organism;
 CC antisense oligonucleotides complementary to AAF76023-AAF76031 are
 CC particularly preferred for this purpose. The second method involves
 CC providing additional vanH promoter sequences which are not operatively
 CC coupled to a vancomycin resistance gene, so that the phosphorylated vanR
 CC gene product (which induces vanH promoter activity) is competitively
 CC sequestered. Both methods are able to restore antibiotic susceptibility
 CC in glycopeptide resistant enterococci. The methods of the invention are
 CC useful for reducing vancomycin resistance in a vancomycin resistant
 CC organism, particularly *Enterococcus faecium* and *Enterococcus faecalis*,
 CC but also in other Gram-positive bacteria such as *Staphylococcus* sp. and
 CC *Streptococcus* sp., to which *Enterococcus faecium* and *Enterococcus*
 CC faecalis have the potential to transfer resistance determinants. The

CC antisense molecules are useful in the treatment of infection and
 CC colonisation by vancomycin resistant enterococci and other clinically
 CC significant pathogens, and may be used for the ex vivo eradication of
 CC vancomycin-resistant enterococci from frequently colonised settings, such
 CC as intensive care units, haemodialysis units, and chronic care facilities
 CC ; for the in vivo clearance of vancomycin-resistant enterococci from
 CC colonised gastrointestinal or genitourinary tracts of animals, including
 CC humans; and in primary or adjuvant therapy for vancomycin-resistant
 CC enterococcal infections. The gene based strategy targets key vancomycin
 CC resistance determinants and results in restoration of vancomycin
 CC susceptibility in previously glycopeptide-resistant enterococci. The
 CC present sequence represents the Enterococcus faecium Vana gene cluster
 SQ Sequence 10851 BP; 3392 A; 1962 C; 2237 G; 3260 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 10851;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCGATCCTGTTTGTGTAAGCCGCGC 27
 |||||
 Db 7472 CCGATCCTGTTTGTGTAAGCCGCGC 7498

RESULT 22
 ACA22997
 ID ACA22997 standard; DNA; 1071 BP.

ACA22997;

19-JUN-2003 (first entry)

Prokaryotic essential gene #4654.

Antisense; ds; prokaryotic essential gene; cell proliferation;
 drug design; gene.

Borrelia burgdorferi.

MO200277183-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.

WPI: 2003-023926/02.

P-PSDB; ABU19127.

New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 10867; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1071 BP; 335 A; 127 C; 198 G; 411 T; 0 U; 0 Other;

Query Match 77.0%; Score 20.8; DB 8; Length 1071;
 Best Local Similarity 91.7%; Pred. No. 21;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 CCGATCCTGTTTGTGTAAGCCGCGC 25
 |||||
 Db 498 CCGATCCTGTTTGTGTAAGCCGCGC 521

RESULT 23

AAK20248_07
 Continuation (8 of 10) of AAK20248 from base 700001 (Borrelia burgdorferi polynucleotide

MP Sequence Split Into 10 fragments LOCUS AAK20248 Accession AAK20248

MP	Fragment Name	Begin	End
MP	AAK20248_00	1	110000
MP	AAK20248_01	100001	210000
MP	AAK20248_02	200001	310000
MP	AAK20248_03	300001	410000
MP	AAK20248_04	400001	510000
MP	AAK20248_05	500001	610000
MP	AAK20248_06	600001	710000
MP	AAK20248_07	700001	810000
MP	AAK20248_08	800001	910000
MP	AAK20248_09	900001	910715

Query Match 77.0%; Score 20.8; DB 2; Length 110000;
 Best Local Similarity 91.7%; Pred. No. 41;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 CCGATCCTGTTTGTGTAAGCCGCGC 25
 |||||
 Db 10177 CCGATCCTGTTTGTGTAAGCCGCGC 10200

RESULT 24
 ADO47266/C

ID ADO47266 standard; DNA; 555 BP.

ADO47266;

15-JUN-2004 (first entry)

Enterococcus vancomycin resistance gene, vanB ENEVANB2A.

Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;

gene; ds; hospital acquired infection; VRB;
 fluorescence resonance energy transfer; FRFT.

XX OS Enterococcus sp.
XX PR US2004058336-A1.
XX PN
XX PD 25-MAR-2004.
XX PF 25-SEP-2002; 2002US-00254260.
XX PR 25-SEP-2002; 2002US-00254260.
XX PA (COCK/) COCKERILL F R.
XX PA (SLOAN/) SLOAN L M.
XX PI Cockerill FR, Sloan LM;
XX DR WPI; 2004-268785/25.
XX PT Detecting presence or absence of vancomycin-resistant enterococci in
XX PT biological sample from individual comprises using real time polymerase
XX PT chain reaction.
XX PS Disclosure; SEQ ID NO 20; 23pp; English.
XX CC The invention relates to detecting the presence or absence of vancomycin-
XX CC resistant enterococci (VRE) in a sample, comprising performing a cycling
XX CC step by amplifying a sample with pair of vanA or vanB primers and
XX CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
XX CC donor and acceptor fluorescent group, respectively, detecting
XX CC fluorescence resonance energy transfer (FRET), where the presence of FRET
XX CC indicates presence of VRE. Also included is an article of manufacture,
XX CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
XX CC and a donor fluorescent group and a corresponding fluorescent group. The
XX CC method is useful for detecting the presence or absence of vancomycin-
XX CC resistant enterococci in a biological sample, e.g. stool samples, anal or
XX CC perirectal swabs, blood and body fluids from an individual. The method
XX CC replaces standard culture methods and reduces the cost. The method
XX CC provides rapid vancomycin resistant enterococcus real time PCR assay
XX CC which is useful for beginning the antimicrobial therapy immediately to
XX CC treat hospital acquired infection. The present sequence is an
XX CC enterococcal vanB, vancomycin resistance gene.
XX SQ Sequence 555 BP; 132 A; 161 C; 115 G; 145 T; 0 U; 2 Other;
XX
XX Query Match 76.3%; Score 20.6; DB 12; Length 555;
XX Best Local Similarity 85.2%; Pred. No. 23;
XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
XX Db 391 CTTACCTGTCTTGTGTAAGCCGCGC 365
XX
XX RESULT 25
XX ADO47264/C
XX ID ADO47264 standard; DNA; 556 BP.
XX AC ADO47264;
XX DT 15-JUL-2004 (first entry)
XX DE Enterococcus vancomycin resistance gene, vanB ENEVANB.
XX OS
XX KM Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
XX KM gene; ds; hospital acquired infection; VRE;
XX KM fluorescence resonance energy transfer; FRET.
XX OS Enterococcus sp.
XX XX US2004058336-A1.
XX PN
XX PD 25-MAR-2004.
XX PA (COCK/) COCKERILL F R.
XX PA (SLOAN/) SLOAN L M.

PF 25-SEP-2002; 2002US-00254260.
XX 25-SEP-2002; 2002US-00254260.
XX XX
XX PA (COCK/) COCKERILL F R.
XX PA (SLOAN/) SLOAN L M.
XX PI Cockerill FR, Sloan LM;
XX DR WPI; 2004-268785/25.
XX XX
XX PT Detecting presence or absence of vancomycin-resistant enterococci in
XX PT biological sample from individual comprises using real time polymerase
XX PT chain reaction.
XX PS Disclosure; SEQ ID NO 18; 23pp; English.
XX CC The invention relates to detecting the presence or absence of vancomycin-
XX CC resistant enterococci (VRE) in a sample, comprising performing a cycling
XX CC step by amplifying a sample with pair of vanA or vanB primers and
XX CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
XX CC donor and acceptor fluorescent group, respectively, detecting
XX CC fluorescence resonance energy transfer (FRET), where the presence of FRET
XX CC indicates presence of VRE. Also included is an article of manufacture,
XX CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
XX CC and a donor fluorescent group and a corresponding fluorescent group. The
XX CC method is useful for detecting the presence or absence of vancomycin-
XX CC resistant enterococci in a biological sample, e.g. stool samples, anal or
XX CC perirectal swabs, blood and body fluids from an individual. The method
XX CC replaces standard culture methods and reduces the cost. The method
XX CC provides rapid vancomycin resistant enterococcus real time PCR assay
XX CC which is useful for beginning the antimicrobial therapy immediately to
XX CC treat hospital acquired infection. The present sequence is an
XX CC enterococcal vanB, vancomycin resistance gene.
XX SQ Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;
XX
XX Query Match 76.3%; Score 20.6; DB 12; Length 556;
XX Best Local Similarity 85.2%; Pred. No. 23;
XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
XX Db 392 CTTACCTGTCTTGTGTAAGCCGCGC 366
XX
XX RESULT 26
XX ADO47262/C
XX ID ADO47262 standard; DNA; 556 BP.
XX AC ADO47262;
XX DT 15-JUL-2004 (first entry)
XX DE E. faecalis vancomycin resistance gene, vanB EFT94526.
XX OS
XX KM Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
XX KM gene; ds; hospital acquired infection; VRE;
XX KM fluorescence resonance energy transfer; FRET.
XX OS Enterococcus faecalis.
XX OS US2004058336-A1.
XX PN
XX PD 25-MAR-2004.
XX PF 25-SEP-2002; 2002US-00254260.
XX PR 25-SEP-2002; 2002US-00254260.
XX XX
XX PA (COCK/) COCKERILL F R.
XX PA (SLOAN/) SLOAN L M.

PI Cockerill FR, Sloan LM;
XX
XX WPI; 2004-268785/25.
DR
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
XX Disclosure; SEQ ID NO 15; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 133 A; 162 C; 116 G; 145 T; 0 U; 0 Other;
XX
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
Db 392 CCTACCTGTCTTTGTGAAGCGGCGAC 366
XX
RESULT 27
ADO47263/c
ID ADO47263 standard; DNA; 556 BP.
XX
AC ADO47263;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94527.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KM gene; de; hospital acquired infection; VRE;
KM fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
XX US2004058336-A1.
PN
XX 25-MAR-2004.
PD
XX 25-SEP-2002; 2002US-00254260.
PP
XX 25-SEP-2002; 2002US-00254260.
PR
XX (COCK/) COCKERILL F R.
PA (SLOAN) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
XX WPI; 2004-268785/25.
DR
XX
XX Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.

XX
XX Disclosure; SEQ ID NO 17; 23pp; English.
XX
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;
XX
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
Db 392 CCTACCTGTCTTTGTGAAGCGGCGAC 366
XX
RESULT 28
ADO47261/c
ID ADO47261 standard; DNA; 556 BP.
XX
AC ADO47261;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94529.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KM gene; de; hospital acquired infection; VRE;
KM fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
XX US2004058336-A1.
PN
XX 25-MAR-2004.
PD
XX 25-SEP-2002; 2002US-00254260.
PP
XX 25-SEP-2002; 2002US-00254260.
PR
XX (COCK/) COCKERILL F R.
PA (SLOAN) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
XX WPI; 2004-268785/25.
DR
XX
XX Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
XX Disclosure; SEQ ID NO 14; 23pp; English.
XX
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridizing the sample with a pair of vanA or vanB probes, labelled with

CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRB. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
Db 392 CCTACCTGTTTGTGTAAGCCGCGCAC 366
RESULT 29
ADO47265/c
ID ADO47265 standard; DNA; 556 BP.
XX
AC ADO47265;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU72704.
XX
KM Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KM gene; ds; hospital acquired infection; VRB;
KM fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOAN/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
PT
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 19; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRB. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or

CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 134 A; 158 C; 117 G; 147 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
Db 392 CCTACCTGTTTGTGTAAGCCGCGCAC 366
RESULT 30
ADO47260/c
ID ADO47260 standard; DNA; 556 BP.
XX
AC ADO47260;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94528.
XX
KM Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KM gene; ds; hospital acquired infection; VRB;
KM fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOAN/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
PT
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 13; 23pp; English.
XX
CC The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRB. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX

SO Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
DB 392 CCTACCTGCTTTGTGAAGCGGCGAC 366

RESULT 31

ADO47259/C
ID ADO47259 standard; DNA; 556 BP.

AC ADO47259;

DT 15-JUN-2004 (first entry)

DE E. faecalis vancomycin resistance gene, vanB BFU94530.

XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;

KW gene; ds; hospital acquired infection; VRB;

KW fluorescence resonance energy transfer; FRBT.

XX Enterococcus faecalis.

OS US2004058336-A1.

PN 25-MAR-2004.

PD 25-SEP-2002; 2002US-00254260.

PP 25-SEP-2002; 2002US-00254260.

PR (COCK/) COCKERILL F R.

PA (SLOAN/) SLOAN L M.

PI Cockerill FR, Sloan LM;

DR WPI; 2004-268785/25.

PT Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase chain reaction.

PS Disclosure; SEQ ID NO 16; 23bp; English.

XX The invention relates to detecting the presence or absence of vancomycin-resistant enterococci (VRE) in a sample, comprising performing a cycling step by amplifying a sample with pair of vanA or vanB primers and

CC hybridizing the sample with a pair of vanA or vanB probes, labelled with donor and acceptor fluorescent group, respectively, detecting

CC fluorescence resonance energy transfer (FRET), where the presence of FRET

CC indicates presence of VRE. Also included is an article of manufacture,

CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes

CC and a donor fluorescent group and a corresponding fluorescent group. The

CC method is useful for detecting the presence or absence of vancomycin-

CC resistant enterococci in a biological sample, e.g. stool samples, anal or

CC perirectal swabs, blood and body fluids from an individual. The method

CC replaces standard culture methods and reduces the cost. The method

CC provides rapid vancomycin resistant enterococcus real time PCR assay

CC which is useful for beginning the antimicrobial therapy immediately to

CC treat hospital acquired infection. The present sequence is an

CC enterococcal vanB, vancomycin resistance gene.

DB 392 CCTACCTGCTTTGTGAAGCGGCGAC 366

RESULT 32
AAQ69230
ID AAQ69230 standard; DNA; 589 BP.

AC AAQ69230;

DT 25-MAR-2003 (revised)

DT 23-FEB-1995 (first entry)

DE Enterococcus faecalis vanB gene (internal, amplified fragment).

XX Gram positive bacteria; inducible glycopeptide resistance; vancomycin;

KW teicoplanin; antibiotic; vanB gene; ds.

OS Enterococcus faecalis.

XX Key Location/Qualifiers

FT misc_feature 2..589

FT /note= "amplified internal fragment of vanB gene"

PF 18-DEC-1992; 92PR-00015671.

PR 18-DEC-1992; 92PR-00015671.

PA (INSP) INST PASTEUR.

PI Arthur M, Dutka-Malen S, Evers S, Courvalin P;

DR P-PSDB; AAR57150.

XX WPI; 1994-227159/28.

PT New protein VanB involved in bacterial resistance to glyco-peptide(s) -

XX esp vancomycin, and related nucleic acid, vectors, transformed cells and

XX antibodies, for in vitro detection of resistant strains.

PS Claim 8; Page 28; 39pp; French.

XX The protein encoded by the vanB gene is implicated in resistance of Gram-

CC positive bacteria to glycopeptides, particularly to vancomycin. This

CC resistance is inducible by Vancomycin but not by teicoplanin. Sequence

CC AAQ69230 is a claimed internal fragment of the vanB gene. (Updated on 25-

CC MAR-2003 to correct PN field.)

XX Sequence 589 BP; 163 A; 124 C; 166 G; 136 T; 0 U; 0 Other;

QY Query Match 76.3%; Score 20.6; DB 2; Length 589;

DB Best Local Similarity 85.2%; Pred. No. 23;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCGGCGC 27

DB 165 CCTACCTGCTTTGTGAAGCGGCGAC 191

RESULT 33

ADY59941
ID ADY59941 standard; DNA; 630 BP.

AC ADY59941;

DT 02-JUN-2005 (first entry)

XX Enterococcus faecalis vanB DNA sequence SEQ ID NO:15.

KM	DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX	
OS	Enterococcus faecalis.
XX	
PN	US2005058985-A1.
PD	17-MAR-2005.
XX	
PP	12-SEP-2003; 2003US-00661094.
XX	
PR	12-SEP-2003; 2003US-00661094.
PA	(DODG/) DODGSON K J.
XX	
Pt	Dodgson KJ;
XX	
DR	WPI; 2005-222218/23.
PT	Detecting vana and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vana-and/or vanB-specific oligonucleotide probes or primers.
XX	
PS	Example 1; SEQ ID NO 15; 33pp; English.
CC	The invention relates to a method for detecting vancomycin resistance gene vana and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vana- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the vana gene, or its complement or portion, or an oligonucleotide comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonucleotide hybridizes under stringent hybridization conditions to vana or vanB DNA, and (2) a kit comprising one or more oligonucleotide(s) specific for a vana gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vana and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products requiring microbiological control. The present sequence represents an Enterococcus faecalis vanB nucleotide sequence from the present invention.
CC	
CC	
CC	
SQ	Sequence 630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;
	Query Match 76.3%; Score 20.6; DB 14; Length 630;
	Best Local Similarity 85.2%; Pred. No. 24;
	Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY	1 CCTATCCTGTTTTGTTAAGCGGGGC 27 Db 185 CCTACCTGTCTTTGTGAAGCGGCAC 211
RESULT 34	
ID	ADYS9942 standard; DNA; 783 BP.
AC	ADYS9942;
DT	02-JUN-2005 (first entry)
DB	Enterococcus faecalis vanB DNA sequence SEQ ID NO.16.
XX	
XX	DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
OS	Enterococcus faecalis.
XX	
PN	US2005058985-A1.

XX 17-MAR-2005.
 PD 12-SEP-2003; 2003US-00661094.
 PF 12-SEP-2003; 2003US-00661094.
 PR 12-SEP-2003; 2003US-00661094.
 PS (DODG/) DODGSON K J.
 PA (DODG/) DODGSON K J.
 P1 Dodgson KJ;
 DR WPI; 2005-222218/23.
 PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
 PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
 PT and/or vanB-specific oligonucleotide probes or primers.
 PS Example 1; SEQ ID NO 16; 33pp; English.
 XX The invention relates to a method for detecting vancomycin resistance
 CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
 CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
 CC probe or primer, and detecting or determining the presence or amount of
 CC hybrid formation or amplified nucleic acid. Also described: (1) an
 CC oligonucleotide composition comprising a first oligonucleotide comprising
 CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
 CC 898-917 of the vanA gene, or its complement or portion, or an
 CC oligonucleotide comprising sequences substantially corresponding to
 CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
 CC complement or portion, where the oligonucleotide hybridizes under
 CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
 CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
 CC vanB gene in a test sample, comprising the oligonucleotide mentioned
 CC above. The method and kit are useful for detecting and/or amplifying
 CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
 CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
 CC They may also be used in other industrial purposes, such as for quality
 CC control of food, water, pharmaceutical products or other products
 CC requiring microbiological control. The present sequence represents an
 CC *Enterococcus faecalis* vanB nucleotide sequence from the present
 CC invention.
 SQ Sequence 783 BP; 215 A; 166 C; 223 G; 179 T; 0 U; 0 Other;
 XX
 Query Match 76.3%; Score 20.6; DB 14; Length 783;
 Best Local Similarity 85.2%; Pred. No. 24;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
 Db |||||
 392 CCTACCCCTGCTTGTGTAAGCCGCGC 418
 RESULT 35
 ID AAH01126
 XX AAH01126 standard; DNA; 801 BP.
 XX AAH01126;
 AC
 XX 24-JUL-2001 (first entry)
 DT
 XX
 DE *Enterococcus faecium* nucleotide sequence SEQ ID NO:1117.
 XX
 XX Species specific; genus specific; family specific; probe; detection;
 KW identification; algal; archaeal; bacterial; fungal; parasitical;
 KW microorganism; diagnosis; translation elongation factor Tu; toxin;
 KW translation elongation factor G; RecA recombinase; resistance;
 KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KW primer; de.
 XX
 OS *Enterococcus faecium*.
 XX
 PN WO200123604-A2.

XX 05-APR-2001.
 XX 28-SEP-2000; 2000MO-CA001150.
 XX 28-SEP-1999; 99CA-02283458.
 XX 19-MAR-2000; 2000CA-02307010.
 XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 XX Bergeron MG, Bolashinot M, Huletsky A, Menard C, Ouellette M;
 XX Picard RJ, Roy PH;
 XX WPI; 2001-245006/25.
 XX Nucleic acid sequences are used to generate universal probes and primers
 XX PT which can be used to identify and detect the presence of algal, archaeal,
 XX PT bacterial, fungal and parasitological species in a test sample.
 XX Disclosure; Page 1027; 1580pp; English.

XX The present invention describes a method for generating a repository of
 XX CC nucleic acids of tuf, fts, atp and/or recA genes from which probes
 XX CC and/or primers are derived. The method comprises amplifying the nucleic
 XX CC acids of determined algal, archaeal, bacterial, fungal and parasitological
 XX CC species with a combination of defined primer pairs. The method can be
 XX CC used for producing probes and/or primers for detecting one or more
 XX CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 XX CC parasites, for universal detection and for specific and ubiquitous
 XX CC detection and identification of an algal, archaeal, bacterial, fungal and
 XX CC parasitological species, genus, family and group. A nucleic acid (I) obtained
 XX CC using the method of the invention can be used for the universal detection
 XX CC of any bacterium, fungus or parasite in a sample and for the detection of
 XX CC at least one antimicrobial agent resistance gene or at least one toxin
 XX CC gene. hexa nucleic acids are used for the specific and ubiquitous
 XX CC detection and for identification of Streptococcus pneumoniae. (I) can be
 XX CC used to design a therapeutic agent which is effective against
 XX CC microorganisms. Microbial species or genus or family or phylum or group
 XX CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
 XX CC Corynebacterium sp., Enterobacteriaceae group, Bacillus coli,
 XX CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
 XX CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 XX CC results than substrate specificity tests as results can be determined in
 XX CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 XX CC represent nucleotide sequences and primers/probes which are given in the
 XX CC exemplification of the present invention

XX Sequence 801 BP; 215 A; 169 C; 235 G; 182 T; 0 U; 0 Other;

XX Query Match 76.3%; Score 20.6; DB 4; Length 801;
 XX Best Local Similarity 85.2%; Pred. No. 25;
 XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
 DB 389 CCTACCTGTCTTGTGTAAGCGGCGC 415

XX RESULT 36
 XX ADY59937/c
 XX ID ADY59937 standard; DNA; 801 BP.
 XX AC ADY59937;
 XX XX

XX 02-JUN-2005 (first entry)

XX Enterococcus faecium vanB DNA sequence SEQ ID NO:11.

XX DNA detection; antibiotic-resistance; vancomycin; vanB; de.

XX Enterococcus faecium.

XX US2005058985-A1.

XX 17-MAR-2005.
 XX 12-SEP-2003; 2003US-00661094.
 XX 12-SEP-2003; 2003US-00661094.
 XX (DODG/) DODGSON K J.
 XX Dodgson KJ;
 XX WPI; 2005-222218/23.
 XX Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
 XX PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
 XX PT and/or vanB-specific oligonucleotide probes or primers.
 XX Example 1; SEQ ID NO 11; 33pp; English.

XX The invention relates to a method for detecting vancomycin resistance
 XX CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
 XX CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
 XX CC probe or primer, and detecting or determining the presence or amount of
 XX CC hybrid formation or amplified nucleic acid. Also described: (1) an
 XX CC oligonucleotide composition comprising a first oligonucleotide comprising
 XX CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
 XX CC 898-917 of the vanA gene, or its complement or portion, or an
 XX CC oligonucleotide comprising sequences substantially corresponding to
 XX CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
 XX CC complement or portion, where the oligonucleotide hybridizes under
 XX CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
 XX CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
 XX CC vanB gene in a test sample, comprising the oligonucleotide mentioned
 XX CC above. The method and kit are useful for detecting and/or amplifying
 XX CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
 XX CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
 XX CC They may also be used in other industrial purposes, such as for quality
 XX CC control of food, water, pharmaceutical products or other products
 XX CC requiring microbiological control. The present sequence represents an
 XX CC Enterococcus faecium vanB nucleotide sequence from the present invention.

XX Sequence 801 BP; 181 A; 226 C; 169 G; 225 T; 0 U; 0 Other;

XX Query Match 76.3%; Score 20.6; DB 14; Length 801;
 XX Best Local Similarity 85.2%; Pred. No. 25;
 XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
 DB 413 CCTACCTGTCTTGTGTAAGCGGCGC 387

XX RESULT 37
 XX ADY59940/c
 XX ID ADY59940 standard; DNA; 801 BP.
 XX AC ADY59940;
 XX XX

XX 02-JUN-2005 (first entry)

XX Enterococcus faecium vanB DNA sequence SEQ ID NO:14.

XX DNA detection; antibiotic-resistance; vancomycin; vanB; de.

XX Enterococcus faecium.

XX US2005058985-A1.

XX 17-MAR-2005.

XX 12-SEP-2003; 2003US-00661094.

XX 12-SEP-2003; 2003US-00661094.

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XX      (DODG/) DODGSON K J.
XX PA
XX PT Dodgson KJ;
XX DR WPI; 2005-222218/23.
XX XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX XX
PS Example 1, SEQ ID NO 14; 33bp; English.
XX XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 899-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
XX XX
SQ Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other;
XX XX
QY Query Match 76.3%; Score 20.6; DB 14; Length 801;
DB Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
    1 CCTATCCTGTTTGTGAAGCGGGGC 27
    |||||
    413 CCTACCTGTCTTGTGAAGCGGCAC 387
RESULT 38
ADYS9943/C
ID ADYS9943 standard; DNA; 801 BP.
XX AC
XX ADYS9943;
XX DT
DT 02-JUN-2005 (first entry)
XX DB
DB Consensus vanB DNA sequence SEQ ID NO:14.
XX KW
KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
OS Enterococcus faecium.
OS Enterococcus faecalis.
OS Synthetic.
XX PN
PN US2005058985-A1.
XX PD
PD 17-MAR-2005.
XX PF
PF 12-SEP-2003; 2003US-00661094.
XX PR
PR 12-SEP-2003; 2003US-00661094.
PA (DODG/) DODGSON K J.
XX PI
PI Dodgson KJ;
```

```

XX DR WPI; 2005-222218/23.
XX
XX PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
XX PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
XX PT and/or vanB-specific oligonucleotide probes or primers.
XX
XX PS Example 1; SEQ ID NO 17; 33pp; English.
XX
XX CC The invention relates to a method for detecting vancomycin resistance
XX CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
XX CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
XX CC probe or primer, and detecting or determining the presence or amount of
XX CC hybrid formation or amplified nucleic acid. Also described: (1) an
XX CC oligonucleotide composition comprising a first oligonucleotide comprising
XX CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
XX CC 898-917 of the vanA gene, or its complement or portion, or an
XX CC oligonucleotide sequencing sequences substantially corresponding to
XX CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
XX CC complement or portion, where the oligonucleotide hybridizes under
XX CC stringent hybridization conditions to vanA or vanB DNA, and (2) a kit
XX CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
XX CC vanB gene in a test sample, comprising the oligonucleotide mentioned
XX CC above. The method and kit are useful for detecting and/or amplifying
XX CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
XX CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
XX CC They may also be used in other industrial purposes, such as for quality
XX CC control of food, water, pharmaceutical products or other products
XX CC requiring microbiological control. The present sequence represents a
XX CC consensus vanB nucleotide sequence from the present invention.
XX
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XX
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XX Best Local Similarity 85.2%; Pred. No. 25;
XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 CCTATCCTGTTTGTGTTAAGCCGGCGC 27
XX ||||| ||||| ||||| ||||| |||||
XX 413 CCTACCCCTGCTTGTGTAAGCCGGCAC 387
XX
XX RESULT 39
XX ID ADY59939/C
XX ID ADY59939 standard; DNA; 801 BP.
XX
XX AC ADY59939;
XX
XX DT 02-JUN-2005 (first entry)
XX
XX DE Enterococcus faecium vanB DNA sequence SEQ ID NO:13.
XX
XX KM DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
XX OS Enterococcus faecium.
XX
XX PN US2005058985-A1.
XX
XX PD 17-MAR-2005.
XX
XX PF 12-SEP-2003; 2003US-00661094.
XX
XX PR 12-SEP-2003; 2003US-00661094.
XX
XX PA (DODG/) DODGSON K J.
XX
XX FI Dodgson KJ;
XX
XX DR WPI; 2005-222218/23.
XX
XX PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
XX PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
XX PT and/or vanB-specific oligonucleotide probes or primers.

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XX Example 1; SEQ ID NO 13; 33pp; English.
XX The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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AC ADY59936;
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DT 02-JUN-2005 (first entry)
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KM DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
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OS Enterococcus faecium.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PF 12-SEP-2003; 2003US-00661094.
XX
PR 12-SEP-2003; 2003US-00661094.
XX
PA (DODG/) DODGSON K J.
XX
PI Dodgson KJ;
XX
DR WPI; 2005-222218/23.
XX
PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
PS Example 1; SEQ ID NO 10; 33pp; English.
XX
CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide

CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ Sequence 801 BP; 182 A; 235 C; 169 G; 215 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
DB 413 CCTACCTGTCTTTGTGAAGCGGCGAC 387
Search completed: April 9, 2006, 06:41:33
Job time : 387.134 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 06:01:49 ; Search time 1049.14 Seconds

(without alignments)
1462.883 Million cell updates/sec

Title: US-10-661-094-3

Perfect score: 27
Sequence: 1 cctatccgttttgcgaagccgcgc 27

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database :

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1: gb_ba:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	27	100.0	1029	6	AR035505 Sequence
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5	27	100.0	1032	1	AY648035 Penibacti
6	27	100.0	1032	1	AY648035 Penibacti
7	27	100.0	1032	1	AY648035 Penibacti
8	27	100.0	1032	1	AY648035 Penibacti
9	27	100.0	1034	6	CO797595 Sequence
10	27	100.0	1232	6	AX110321 Sequence
11	27	100.0	1232	6	AX110321 Sequence
12	27	100.0	1237	6	AX110319 Sequence
13	27	100.0	1241	6	AX110316 Sequence
14	27	100.0	1249	6	AX110317 Sequence
15	27	100.0	1263	6	AX110320 Sequence
16	27	100.0	1265	6	AX110323 Sequence
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19	27	100.0	1768	1	EF9VANA6
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ALIGNMENTS

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VERSION      AY754011.1  GI:57790303
KEYWORDS
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ORGANISM     Enterococcus faecium
              Enterococcus faecium
              Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
              Enterococcus.
REFERENCE    1 (bases 1 to 614)
              Khudaler,B.Y., Shafiani,S., Tewari,R. and Taneja,N.
              Detection and molecular characterization of vancomycin resistance
              genes from clinical strains of Enterococci
              Unpublished
              2 (bases 1 to 614)
              Khudaler,B.Y., Shafiani,S., Tewari,R. and Taneja,N.
              Direct Submission
              Submitted (18-SEP-2004) Biotechnology, Panjab University,
              Sector-14, Chandigarh, U.T 160014, India
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[illegible]

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DEFINITION	Sequence 3 from patent US 5871910.
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VERSION	AR035505.1 GI:5952173
KEYWORDS	.
SOURCE	. Unknown. . Unclasiified.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 1029)
AUTHORS	Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
TITLE	Probes for the detection of nucleotide sequences implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria
JOURNAL FEATURES	Patent: US 5871910-A 3 16-FEB-1999; Location/Qualifiers
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DB 494 CCTATCCTGTTTGTGTAAGCCGCGC 520

RESULT 4
LOCUS BD181846
DEFINITION Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis.

ACCESSION BD181846
VERSION BD181846.1 GI:30792764
KEYWORDS JP 2002320494-A/2.
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 1029)
AUTHORS Arthur, M., Dukcamalen, S., Molina, C. and Courvalin, P.
TITLE Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
JOURNAL Institut Pasteur
COMMENT OS Bacteria
PN JP 2002320494-A/2
PD 05-NOV-2002
PR 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PI MICHEL, ARTHUR, SYLVIE, DUKTA-MALEN, CATHERINE, MOLINA, PATRICE, COURVALIN

FEATURES
SOURCE CC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10, PC C12Q1/04, C12Q1/68, G01N33/53, G01N33/569//C12P21/08, PC C12Q1/04, C12R1/01, C12Q1/68, C12R1/01, C12N15/00, C12N5/00 CC Polypeptides implicated in the expression of resistance to CC glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
CC in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
CC these polypeptides and use for diagnosis
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QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
DB 494 CCTATCCTGTTTGTGTAAGCCGCGC 520

RESULT 5
LOCUS AY648035
DEFINITION Paenibacillus thiaminolyticus D-alanyl-D-alanine ligase gene, complete cds.

ACCESSION AY648035
VERSION AY648035.1 GI:50082936
KEYWORDS Paenibacillus thiaminolyticus
SOURCE Paenibacillus thiaminolyticus
ORGANISM Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
REFERENCE 1 (bases 1 to 1032)
AUTHORS Guardabassi, L., Christensen, H., Hasman, H. and Dalsgaard, A.
TITLE Members of the Genus Paenibacillus and Rhodococcus Harbor Genes Homologous to Enterococcal Glycopeptide Resistance Genes vanA and vanB

JOURNAL Antimicrob. Agents Chemother. 48 (12), 4915-4918 (2004)
PUBMED 15561881
REFERENCE 2 (bases 1 to 1032)
AUTHORS Guardabassi, L., Hasman, H., Christensen, H. and Dalsgaard, A.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2004) Veterinary Pathobiology, The Royal Veterinary and Agricultural University, Stigboejlen 4, Frederiksberg C 1870, Denmark

FEATURES
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/protein_id="AAT70090.1"
/db_xref="GI:50082937"
/translation="MNRKVALIFPGGSEEDHVSARSAREIANIDNEKTEPLYTIGT KRWKMEKPKAEWENSCYSAVSPDKKHGLVXNNREYIHVDVAFVLGKS GEDGSIQGLFELSGIPYGCIDQSSAICMKSILTYTAKAGATPDPTVTKDKKA I0AFTYPPVKKPARSGSSGVKXNGADELDALIESAKQYDSKILTEQVILGCEVCA VLANSSELI VGEVDQIRLQDGI FRIHQEAPKESNAVTTIPADISVVRGRLQETA KLYKALGCRGSRVDMFLQDNGSIVLNEVTLPGFTSYSRVRRMVAAGITLPELID RLVALAKG"

ORIGIN
Query Match 100.0%; Score 27; DB 1; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
DB 494 CCTATCCTGTTTGTGTAAGCCGCGC 520

RESULT 6
LOCUS AY648698
DEFINITION Paenibacillus apiarius D-alanyl-D-alanine ligase gene, complete cds.

ACCESSION AY648698
VERSION AY648698.1 GI:50082942
KEYWORDS Paenibacillus apiarius
SOURCE Paenibacillus apiarius
ORGANISM Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
REFERENCE 1 (bases 1 to 1032)
AUTHORS Guardabassi, L., Christensen, H., Hasman, H. and Dalsgaard, A.
TITLE Members of the Genus Paenibacillus and Rhodococcus Harbor Genes Homologous to Enterococcal Glycopeptide Resistance Genes vanA and vanB

JOURNAL Antimicrob. Agents Chemother. 48 (12), 4915-4918 (2004)
PUBMED 15561881
REFERENCE 2 (bases 1 to 1032)
AUTHORS Guardabassi, L., Hasman, H., Christensen, H. and Dalsgaard, A.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-2004) Veterinary Pathobiology, The Royal Veterinary and Agricultural University, Stigboejlen 4, Frederiksberg C 1870, Denmark

FEATURES
SOURCE 1. 1032
/organism="Paenibacillus apiarius"
/mol_type="genomic DNA"
/strain="PA-828"
/db_xref="taxon:46240"
1. 1032
/codon_start=1
/transl_table=11
/product="D-alanyl-D-alanine ligase"
/protein_id="AAT70093.1"

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/db_xref="GI:50082943"
/translation="MYRKIALIFGGGSEHDVSVKAKRIANNINTEKYEPIYIGIT
RSGVWTCERPCMDNDNENRASAIVLSPDKRMHGLTMRDGYOIORIDAFASTLHRS
GEGDAIQGLFELSGIPYVCGDIOSSAYCNDKSLATIIAKRDGATPEFWYINCDHPA
AAAFYVPAVKPARSGSSYGKVNAGADEIDAAIESARQYDSKILIQAVLGEVCA
VLGNSSELIVGEVDQIRLOHGFRIHQEAPKESNAVTTIPADLSAERGRIRDTA
KRIYKALGCGRLARVDMFLQDNGRIYLVENVTLPGFTSYSRPRMVAAGITLPELID
RLVLVLKNG"

ORIGIN

Query Match      100.0%; Score 27; DB 1; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
    |||||
Db 494 CCTATCCTGTTTGTGTTAAGCCGCGC 520

RESULT 7
LOCUS AX085668 1032 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 21 from Patent WO0112803.
ACCESSION AX085668
VERSION AX085668.1 GI:13275654
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
REFERENCE 1
AUTHORS Inouye, R.T., Torres-Viera, C., Moellering, R., Gold, H. and
          Eliopoulos, G.M.
TITLE Methods and compositions for restoring antibiotic susceptibility in
          glycopeptide-resistant Enterococcus
JOURNAL Patent: WO 0112803-A 21 22-FEB-2001;
          Beth Israel Deaconess Medical Center, Inc. (US)
FEATURES
    source
        location/Qualifiers
            1..1032
            /organism="Enterococcus faecium"
            /mol_type="unassigned DNA"
            /db_xref="taxon:1352"

ORIGIN

Query Match      100.0%; Score 27; DB 6; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
    |||||
Db 494 CCTATCCTGTTTGTGTTAAGCCGCGC 520

RESULT 8
LOCUS AX11560 1032 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 2293 from Patent WO0123604.
ACCESSION AX11560
VERSION AX11560.1 GI:13927852
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
REFERENCE 1
AUTHORS Bergeron, M.G., Bolesinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
          Picard, F.J. and Roy, P.H.
TITLE Highly conserved genes and their use to generate probes and primers
          for detection of microorganisms
JOURNAL Patent: WO 0123604-A 2293 05-APR-2001;
          Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
    source
        location/Qualifiers
            1..1032

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/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="BM4147"
/db_xref="taxon:1352"

ORIGIN

Query Match      100.0%; Score 27; DB 6; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
    |||||
Db 494 CCTATCCTGTTTGTGTTAAGCCGCGC 520

RESULT 9
LOCUS CQ797595 1034 bp DNA linear PAT 20-APR-2004
DEFINITION Sequence 9 from Patent EP1408120.
ACCESSION CQ797595
VERSION CQ797595.1 GI:46425887
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
REFERENCE 1
AUTHORS Cockerill, P.R. and Sloan, L.M.
TITLE Detection of vancomycin-resistant Enterococcus spp
JOURNAL Patent: EP 1408120-A 9 14-APR-2004;
          MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES
    source
        location/Qualifiers
            1..1034
            /organism="Enterococcus faecium"
            /mol_type="unassigned DNA"
            /db_xref="taxon:1352"

ORIGIN

Query Match      100.0%; Score 27; DB 6; Length 1034;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
    |||||
Db 494 CCTATCCTGTTTGTGTTAAGCCGCGC 520

RESULT 10
LOCUS AX110322 1218 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 1055 from Patent WO0123604.
ACCESSION AX110322
VERSION AX110322.1 GI:13926614
KEYWORDS
SOURCE Enterococcus gallinarum
ORGANISM Enterococcus gallinarum
REFERENCE 1
AUTHORS Bergeron, M.G., Bolesinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
          Picard, F.J. and Roy, P.H.
TITLE Highly conserved genes and their use to generate probes and primers
          for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1055 05-APR-2001;
          Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
    source
        location/Qualifiers
            1..1218
            /organism="Enterococcus gallinarum"
            /mol_type="unassigned DNA"
            /strain="R684"
            /db_xref="taxon:1353"

ORIGIN

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Query Match 100.0%; Score 27; DB 6; Length 1218;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
 Db 568 CCTATCCTGTTTGTGTAAGCGGCGC 594

RESULT 11
 AX110321 1232 bp DNA linear PAT 29-MAY-2002
 LOCUS Sequence 1054 from Patent WO0123604.
 DEFINITION AX110321
 ACCESSION AX110321
 VERSION AX110321.1 GI:13926613
 KEYWORDS Enterococcus faecalis
 SOURCE Enterococcus faecalis
 ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.

REFERENCE 1
 AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
 Picard,P.J. and Roy,P.H.
 TITLE Highly conserved genes and their use to generate probes and primers
 JOURNAL for detection of microorganisms
 PATENT: WO 0123604-A 1054 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)
 FEATURES Location/Qualifiers
 source 1..1232
 /organism="Enterococcus faecalis"
 /mol_type="unassigned DNA"
 /db_xref="taxon:1351"
 /note="R610"

ORIGIN
 Query Match 100.0%; Score 27; DB 6; Length 1232;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
 Db 578 CCTATCCTGTTTGTGTAAGCGGCGC 604

RESULT 12
 AX110319 1237 bp DNA linear PAT 29-MAY-2002
 LOCUS Sequence 1052 from Patent WO0123604.
 DEFINITION AX110319
 ACCESSION AX110319
 VERSION AX110319.1 GI:13926611
 KEYWORDS Enterococcus faecium
 SOURCE Enterococcus faecium
 ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.

REFERENCE 1
 AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
 Picard,P.J. and Roy,P.H.
 TITLE Highly conserved genes and their use to generate probes and primers
 JOURNAL for detection of microorganisms
 PATENT: WO 0123604-A 1052 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)
 FEATURES Location/Qualifiers
 source 1..1237
 /organism="Enterococcus faecium"
 /mol_type="unassigned DNA"
 /strain="R492"
 /db_xref="taxon:1352"

ORIGIN
 Query Match 100.0%; Score 27; DB 6; Length 1237;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
 Db 590 CCTATCCTGTTTGTGTAAGCGGCGC 616

RESULT 13
 AX110316 1241 bp DNA linear PAT 29-MAY-2002
 LOCUS Sequence 1049 from Patent WO0123604.
 DEFINITION AX110316
 ACCESSION AX110316
 VERSION AX110316.1 GI:13926608
 KEYWORDS Enterococcus faecium
 SOURCE Enterococcus faecium
 ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.

REFERENCE 1
 AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
 Picard,P.J. and Roy,P.H.
 TITLE Highly conserved genes and their use to generate probes and primers
 JOURNAL for detection of microorganisms
 PATENT: WO 0123604-A 1049 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)
 FEATURES Location/Qualifiers
 source 1..1241
 /organism="Enterococcus faecium"
 /mol_type="unassigned DNA"
 /strain="R690"
 /db_xref="taxon:1352"

ORIGIN
 Query Match 100.0%; Score 27; DB 6; Length 1241;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
 Db 561 CCTATCCTGTTTGTGTAAGCGGCGC 587

RESULT 14
 AX110317 1249 bp DNA linear PAT 29-MAY-2002
 LOCUS Sequence 1050 from Patent WO0123604.
 DEFINITION AX110317
 ACCESSION AX110317
 VERSION AX110317.1 GI:13926609
 KEYWORDS Enterococcus gallinarum
 SOURCE Enterococcus gallinarum
 ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.

REFERENCE 1
 AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
 Picard,P.J. and Roy,P.H.
 TITLE Highly conserved genes and their use to generate probes and primers
 JOURNAL for detection of microorganisms
 PATENT: WO 0123604-A 1050 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)
 FEATURES Location/Qualifiers
 source 1..1249
 /organism="Enterococcus gallinarum"
 /mol_type="unassigned DNA"
 /strain="R691"
 /db_xref="taxon:1353"

ORIGIN
 Query Match 100.0%; Score 27; DB 6; Length 1249;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27

Db 590 CCTATCCTGTTTGTAAAGCCGCGC 616

RESULT 15

AX110320

LOCUS 1263 bp DNA linear PAT 29-MAY-2002

DEFINITION Sequence 1053 from Patent WO0123604.

ACCESSION AX110320

VERSION AX110320.1 GI:13926612

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M., Picard,F.J. and Roy,P.H.

TITLE

Highly conserved genes and their use to generate probes and primers for detection of microorganisms

JOURNAL

Patent: WO 0123604-A 1053 05-APR-2001;

FEATURES

location/Qualifiers

1..1263

/organism="Enterococcus faecium"

/mol_type="unassigned DNA"

/strain="R581"

/db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1263;

Best Local Similarity 100.0%; Pred. No. 0.5;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTAAAGCCGCGC 27

Db 582 CCTATCCTGTTTGTAAAGCCGCGC 608

RESULT 16

AX110323

LOCUS 1265 bp DNA linear PAT 29-MAY-2002

DEFINITION Sequence 1056 from Patent WO0123604.

ACCESSION AX110323

VERSION AX110323.1 GI:13926615

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M., Picard,F.J. and Roy,P.H.

TITLE

Highly conserved genes and their use to generate probes and primers for detection of microorganisms

JOURNAL

Patent: WO 0123604-A 1056 05-APR-2001;

FEATURES

location/Qualifiers

1..1265

/organism="Enterococcus faecium"

/mol_type="unassigned DNA"

/strain="R688"

/db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1265;

Best Local Similarity 100.0%; Pred. No. 0.5;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTAAAGCCGCGC 27

Db 592 CCTATCCTGTTTGTAAAGCCGCGC 618

RESULT 17

AX110324

LOCUS 1269 bp DNA linear PAT 29-MAY-2002

DEFINITION Sequence 1057 from Patent WO0123604.

ACCESSION AX110324

VERSION AX110324.1 GI:13926616

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M., Picard,F.J. and Roy,P.H.

TITLE

Highly conserved genes and their use to generate probes and primers for detection of microorganisms

JOURNAL

Patent: WO 0123604-A 1057 05-APR-2001;

FEATURES

location/Qualifiers

1..1269

/organism="Enterococcus flavescens"

/mol_type="unassigned DNA"

/strain="R689"

/db_xref="taxon:37735"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1269;

Best Local Similarity 100.0%; Pred. No. 0.5;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTAAAGCCGCGC 27

Db 590 CCTATCCTGTTTGTAAAGCCGCGC 616

RESULT 18

AX110318

LOCUS 1272 bp DNA linear PAT 29-MAY-2002

DEFINITION Sequence 1051 from Patent WO0123604.

ACCESSION AX110318

VERSION AX110318.1 GI:13926610

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M., Picard,F.J. and Roy,P.H.

TITLE

Highly conserved genes and their use to generate probes and primers for detection of microorganisms

JOURNAL

Patent: WO 0123604-A 1051 05-APR-2001;

FEATURES

location/Qualifiers

1..1272

/organism="Enterococcus faecium"

/mol_type="unassigned DNA"

/strain="R481"

/db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1272;

Best Local Similarity 100.0%; Pred. No. 0.5;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTAAAGCCGCGC 27

Db 570 CCTATCCTGTTTGTAAAGCCGCGC 596

RESULT 19

EFPVANAG

LOCUS 1768 bp DNA linear BCT 17-JUN-1991

DEFINITION E.faecium plasmid p1816 vana gene for VANA ligase.
 ACCESSION X56895
 VERSION X56895.1 GI:43335
 KEYWORDS D-alanyl-D-alanine ligase; VANA glycopeptide resistance protein;
 vancomycin resistance.
 SOURCE Enterococcus faecium
 ORGANISM Enterococcus faecium
 Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.
 REFERENCE 1 (bases 1 to 1768)
 AUTHORS Dutka-Malen, S., Molina, C., Arthur, M. and Courvalin, P.
 TITLE The VANA glycopeptide resistance protein is related to
 D-alanyl-D-alanine ligase cell wall biosynthesis enzymes
 JOURNAL Mol. Gen. Genet. 224 (3), 364-372 (1990)
 PUBMED 2266943
 REFERENCE 2 (bases 1 to 1768)
 AUTHORS Dutka-Malen, S.
 TITLE Direct Submission
 JOURNAL Submitted (25-FEB-1991) S. Dutka-Malen, Institut Pasteur, Uille des
 Agents Antibacteriens, 28 rue du Dr Roux, Paris Cedex 15, France
 FEATURES
 source
 1.1768
 /organism="Enterococcus faecium"
 /mol_type="genomic DNA"
 /strain="BM4147"
 /db_xref="taxon:1352"
 /plasmid="p1816"
 360..369
 377..1408
 /gene="vana"
 377..1408
 /gene="vana"
 377..1408
 /evidence="experimental"
 /transl_table=1
 /product="VANA ligase"
 /protein_id="CAA40215.1"
 /db_xref="GI:43336"
 /db_xref="GOA:P25051"
 /db_xref="UniProt/Swiss-Prot:P25051"
 /translation="MNRIRKVALIFGCGSEHDVVKAIIRIANIKKKEPIYITIT
 KSGVWMCERKPAEWENDCYSAVLSPPKRGGLVKNHREINHYDVAFSLHRS
 GEGSIOGLFELSGIPVGCIOSSALICMDSLTYIAKXAGIATPAFWINDDPV
 AATFYPPVKPARSGSGSGYKVSADLELYAESARQDSKLLIQAVSGCEVCA
 VIGNSALVAVGVDQIRLOYGIFRIHSEVPEKSENAVITVPADLSAERGIQETA
 KIKYALGCGRLARVDMITQDNGRIVLNVTTLGFTSYSRIPPMMAAGIALPELID
 RLIVLAKG"
 ORIGIN
 Query Match 100.0%; Score 27; DB 1; Length 1768;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTAAAGCCGCGC 27
 Db 870 CCTATCCTGTTTGTAAAGCCGCGC 896
 RESULT 20
 LOCUS CQ797596 1768 bp DNA linear PAT 20-APR-2004
 DEFINITION Sequence 10 from Patent EP1408120.
 ACCESSION CQ797596
 VERSION CQ797596.1 GI:46425888
 KEYWORDS
 SOURCE Enterococcus faecium
 ORGANISM Enterococcus faecium
 Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.
 REFERENCES
 1
 AUTHORS Cockerill, F.R. and Sloan, L.M.
 TITLE Detection of vancomycin-resistant Enterococcus spp
 JOURNAL Patent: EP 1408120-A 10 14-APR-2004;

FEATURES
 source
 location/Qualifiers
 1..1768
 /organism="Enterococcus faecium"
 /mol_type="unassigned DNA"
 /db_xref="taxon:1352"
 /note="vana sequence"
 ORIGIN
 Query Match 100.0%; Score 27; DB 6; Length 1768;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTAAAGCCGCGC 27
 Db 870 CCTATCCTGTTTGTAAAGCCGCGC 896
 RESULT 21
 LOCUS CQ797597 1768 bp DNA linear PAT 20-APR-2004
 DEFINITION Sequence 11 from Patent EP1408120.
 ACCESSION CQ797597
 VERSION CQ797597.1 GI:46425889
 KEYWORDS
 SOURCE Enterococcus faecium
 ORGANISM Enterococcus faecium
 Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.
 REFERENCES
 1
 AUTHORS Cockerill, F.R. and Sloan, L.M.
 TITLE Detection of vancomycin-resistant Enterococcus spp
 JOURNAL Patent: EP 1408120-A 11 14-APR-2004;
 MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
 FEATURES
 source
 1..1768
 /organism="Enterococcus faecium"
 /mol_type="unassigned DNA"
 /db_xref="taxon:1352"
 /note="vana sequence"
 ORIGIN
 Query Match 100.0%; Score 27; DB 6; Length 1768;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTAAAGCCGCGC 27
 Db 870 CCTATCCTGTTTGTAAAGCCGCGC 896
 RESULT 22
 LOCUS CS061873 1768 bp DNA linear PAT 13-APR-2005
 DEFINITION Sequence 1 from Patent WO2005028679.
 ACCESSION CS061873
 VERSION CS061873.1 GI:62553767
 KEYWORDS
 SOURCE Enterococcus faecium
 ORGANISM Enterococcus faecium
 Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.
 REFERENCES
 1
 AUTHORS Dodgson, K.J.
 TITLE Method and kit for identifying vancomycin-resistant enterococcus
 JOURNAL Patent: WO 2005028679-A 1 31-MAR-2005;
 University of Iowa Research Foundation (US); DODGSON, Kirsty Jane
 (US)
 FEATURES
 source
 location/Qualifiers
 1..1768
 /organism="Enterococcus faecium"
 /mol_type="unassigned DNA"
 /db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
|||||
Db 870 CCTATCCTGTTTGTGTTAAGCCGCGC 896

RESULT 23
AX110406 1768 bp DNA linear PAT 29-MAY-2002
LOCUS Sequence 1139 from Patent WO0123604.
DEFINITION AX110406
ACCESSION AX110406.1 GI:13926698
VERSION
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Bolesinoc,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,P.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1139 05-APR-2001;
FEATURES Infectio Diagnostic (I.D.I.) INC. (CA)
source Location/Qualifiers
1. 1768
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="BM4147"
/db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
|||||
Db 870 CCTATCCTGTTTGTGTTAAGCCGCGC 896

RESULT 24
AR089411 2607 bp DNA linear PAT 07-SEP-2000
LOCUS AR089411
DEFINITION Sequence 170 from patent US 5994066.
ACCESSION AR089411
VERSION AR089411.1 GI:10016168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2607)
AUTHORS Bergeron,M.G., Picard,P.J., Ouellette,M. and Roy,P.H.
TITLE Species-specific and universal DNA probes and amplification primers
to rapidly detect and identify common bacterial pathogens and
associated antibiotic resistance genes from clinical specimens for
routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 170 30-NOV-1999;
FEATURES Location/Qualifiers
1. 2607
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 2607;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
|||||
Db 1455 CCTATCCTGTTTGTGTTAAGCCGCGC 1481

RESULT 25
AR093611 2607 bp DNA linear PAT 08-SEP-2000
LOCUS AR093611
DEFINITION Sequence 170 from patent US 6001564.
ACCESSION AR093611
VERSION AR093611.1 GI:10020360
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2607)
AUTHORS Bergeron,M.G., Ouellette,M. and Roy,P.H.
TITLE Species specific and universal DNA probes and amplification primers
to rapidly detect and identify common bacterial pathogens and
associated antibiotic resistance genes from clinical specimens for
routine diagnosis in microbiology laboratories
JOURNAL Patent: US 6001564-A 170 14-DEC-1999;
FEATURES Location/Qualifiers
1. 2607
/organism="unknown"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
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Db 1455 CCTATCCTGTTTGTGTTAAGCCGCGC 1481

RESULT 26
AR035514 2667 bp DNA linear PAT 29-SEP-1999
LOCUS AR035514
DEFINITION Sequence 17 from patent US 5871910.
ACCESSION AR035514
VERSION AR035514.1 GI:5952182
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2667)
AUTHORS Arthur,M., Dutka-Mallen,S., Molina,C. and Courvalin,P.
TITLE Probes for the detection of nucleotide sequences implicated in the
expression of resistance to glycopeptides, in particular in
gram-positive bacteria
JOURNAL Patent: US 5871910-A 17 16-FEB-1999;
FEATURES Location/Qualifiers
1. 2667
/organism="unknown"
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Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1518 CCTATCCTGTTTGTGTTAAGCCGCGC 1544

RESULT 27
BD181855 2667 bp DNA linear PAT 15-MAY-2003
LOCUS BD181855
DEFINITION Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide


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VIERLRGPGCKVLAVRSOSIEANVYVPDELQNSDIVTLLHVPINADTRHIIISHOIO
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 Db 3502 CCTATCCTGTTTGTGTAAGCGCGCGC 3528

RESULT 30
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 LOCUS AR035512 7225 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 15 from patent US 5871910.
 ACCESSION AR035512
 VERSION AR035512.1 GI:5952180
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 7225)
 Arthur, M., Dukta-Malen, S., Molinas, C. and Courvalin, P.
 TITLE Probes for the detection of nucleotide sequences implicated in the
 expression of resistance to glycopeptides, in particular in
 gram-positive bacteria
 JOURNAL Patent: US 5871910-A is 16-FEB-1999;
 FEATURES
 location/Qualifiers
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 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTAAGCGCGCGC 27
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 Db 5016 CCTATCCTGTTTGTGTAAGCGCGCGC 5042

RESULT 31
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 LOCUS BD181853 7225 bp DNA linear PAT 15-MAY-2003
 DEFINITION Polypeptides implicated in the expression of resistance to
 glycopeptides, in particular in gram-positive bacteria, nucleotide
 sequence cod ing for these polypeptides and use for diagnosis.
 ACCESSION BD181853
 VERSION BD181853.1 GI:30792771
 KEYWORDS JP 2002320494-A/9.
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 7225)
 Arthur, M., Dukta-Malen, S., Molinas, C. and Courvalin, P.
 TITLE Polypeptides implicated in the expression of resistance to
 glycopeptides, in particular in gram-positive bacteria, nucleotide
 sequence cod ing for these polypeptides and use for diagnosis
 JOURNAL Patent: JP 2002320494-A 9 05-NOV-2002;
 COMMENT INSTITUTE PASTEUR
 OS Bacteria
 PN JP 2002320494-A/9
 PD 05-NOV-2002 JP 2002045484
 PR 21-FEB-2002 JP 2002045484
 PR 31-OCT-1990 FR 90/13579
 PI MICHEL ARTHUR, SYLVIE DUKTA-MALEN, CATHERINE MOLINAS, PATRICE PI
 COURVALIN
 PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/29, C12N1/21, PC
 C12N5/10, C12Q1/04, C12Q1/68, G01N33/53, G01N33/566, G01N33/569, C12P21/08,
 PC C12Q1/04, C12Q1/01, C12Q1/68, C12R1/01, C12N15/00, C12N5/00 CC
 Polypeptides implicated in the expression of resistance to CC
 glycopeptides,
 CC in particular in gram-positive bacteria, nucleotide sequence
 CC cod ing for
 CC these polypeptides and use for diagnosis
 FH Key location/Qualifiers
 FT source 1..7225
 FT /organism="Bacteria".
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ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 7225;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTAAGCGCGCGC 27
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 Db 5016 CCTATCCTGTTTGTGTAAGCGCGCGC 5042

RESULT 32
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 LOCUS DQ018711 9519 bp DNA linear BCT 31-MAY-2005
 DEFINITION Paenibacillus apiarius strain Pa-B2B glycopeptide resistance vana
 operon, complete sequence; and Btu-like protein gene, partial cds.
 ACCESSION DQ018711
 VERSION DQ018711.1 GI:66731642
 KEYWORDS
 SOURCE Paenibacillus apiarius
 ORGANISM Paenibacillus apiarius
 Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.

REFERENCE 1 (bases 1 to 9519)
AUTHORS Guardabassi, L., Perichon, B., Van Heijenoort, J., Blanc, D. and Courvalin, P.
TITLE Glycopeptide resistance van operons in *Paenibacillus* from soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9519)
AUTHORS Guardabassi, L., Perichon, B., Van Heijenoort, J., Blanc, D. and Courvalin, P.
TITLE Direct Submission
JOURNAL Submitted (26-Apr-2005) Unite des Agents Antibacteriens, Institut Pasteur, 25 rue du Docteur Roux, Paris 75015, France
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Query Match 100.0%; Score 27; DB 1; Length 9519;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTTAAGCCGGCGC 27
Db 4622 CCTATCCTGTTTGTGTTAAGCCGGCGC 4648

RESUT 33
LOCUS DQ018710 9537 bp DNA linear BCT 31-MAY-2005
DEFINITION Paenibacillus thiaminolyticus strain PT-281 putative transposase
and putative GNAI family acetyltransferase genes, complete cds; and
glycopeptide resistance vanA operon, partial sequence.
ACCESSION DQ018710
VERSION DQ018710.1 GI:66731632
SOURCE
ORGANISM Paenibacillus thiaminolyticus
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
1 (bases 1 to 9537)
Guadabassi, L., Perichon, B., Van Heldenort, J., Bianot, D. and
Courvalin, P.
Glycopeptide resistance van operons in Paenibacillus from soil
Unpublished
2 (bases 1 to 9537)
Guadabassi, L., Perichon, B., Van Heldenort, J., Bianot, D. and
Courvalin, P.
Direct Submission
Submitted (26-Apr-2005) Unite des Agents Antibacteriens, Institut
Pasteur, 25 rue du Docteur Roux, Paris 75015, France
FEATURES
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/isolation_source="soil"
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ORIGIN	Query Match 100.0%; Score 27; DB 1; Length 10851; Best Local Similarity 100.0%; Pident. No. 0.37; Indels 0; Gaps 0; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 CCTATCCGTGTTTGTTAAGCCGGCGC 27 			
Db	7472 CCTATCCGTGTTTGTTAAGCCGGCGC 7498			
RESULT 35				
AR035513	10851 bp DNA linear PAT 29-SEP-1999			
LOCUS	AR035513			
DEFINITION	Sequence 16 from patent US 5871910.			
ACCESSION	AR035513			
VERSION	AR035513.1 GI:5952181			
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 10851)			
TITLE	Arthur,M., Duka-Malen,S., Molinas,C. and Courvailln,P. Probes for the detection of nucleotide sequences implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria Patent: US 5871910-A 16 16-FEB-1999; location/Qualifiers 1..10851 /organism="unknown" /mol_type="unassigned DNA"			
JOURNAL				
FEATURES				
source				
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Qy	1 CCTATCCGTGTTTGTTAAGCCGGCGC 27 			

DB 7472 CCTATCCTGTTTGTTAAGCCGCCGC 7498

RESULT 36
LOCUS BD181854
DEFINITION Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis.
ACCESSION BD181854
VERSION BD181854.1 GI:30792772
KEYWORDS JP 2002320494-A/10.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE
AUTHORS Arthur M., Dukcamalen S., Molinas C. and Courvalin P.
TITLE Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
JOURNAL Patent: JP 2002320494-A 10 05-NOV-2002;
INSTITUT PASTEUR

COMMENT
OS Bacteria
PN JP 2002320494-A/10
PD 05-NOV-2002
PF 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PI MICHEL ARTHUR, SYLVIE DUKTA-MALEN, CATHERINE MOLINAS, PATRICE COURVALIN

PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10,
PC C12Q1/04, C12Q1/68, G01N33/53, G01N33/566, G01N33/569//C12P21/08,
PC C12Q1/04, C12R1/01, C12Q1/68, C12R1/01, C12N15/00, C12N5/00 CC
Polypeptides implicated in the expression of resistance to CC
glycopeptides, in gram-positive bacteria, nucleotide sequence
CC in particular in gram-positive bacteria, nucleotide sequence
CC coding for
CC these polypeptides and use for diagnosis
FH Key Location/Qualifiers
FT source 1..10851
FT Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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7472 CCTATCCTGTTTGTTAAGCCGCCGC 7498

RESULT 37
LOCUS AX085648
DEFINITION Sequence 1 from Patent WO0112803.
ACCESSION AX085648
VERSION AX085648.1 GI:13275634
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE
AUTHORS Inouye, R.T., Torres-Viera, C., Moellering, R., Gold, H. and Eliopoulos, G.M.
TITLE Methods and compositions for restoring antibiotic susceptibility in glycopeptide-resistant Enterococcus

JOURNAL Patent: WO 0112803-A 1 22-FEB-2001;
Beth Israel Deaconess Medical Center, Inc. (US)

FEATURES
source
Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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7472 CCTATCCTGTTTGTTAAGCCGCCGC 7498

RESULT 38
LOCUS AF516335
DEFINITION Enterococcus faecium plasmid pUW786 multiple antibiotic resistance gene cluster, complete sequence.
ACCESSION AF516335
VERSION AF516335.1 GI:21886737
KEYWORDS
SOURCE
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE
AUTHORS Werner, G., Klare, I. and Witte, W.
TITLE Multi-resistance gene cluster on a plasmid in a clinical isolate of Enterococcus faecium
JOURNAL unpublished
REFERENCE 1 (bases 1 to 17510)
AUTHORS Werner, G.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Wernigerode Branch, Robert Koch Institute, Bursfelde, Germany

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/db_xref="GI:21886747"
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KILPRVLMVDEFSRHASIEDKMSFICADGEGTGLIDVLPRLKPLRSLYFLGCTNPE
VERFLTDMNAAYFOLTKRVLPNAKVIIDRPHIVSHNQAOENELRIBEMELRAGQGS
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Db 34792 CCTATCCTGTTTGTGTTAAGCCGGCCG 34818

RESULT 40
LOCUS BCY15704 1054 bp DNA linear BCT 18-Apr-2005
DEFINITION *Bacillus circulans* vana gene.
ACCESSION BCY15704
VERSION 1
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
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JOURNAL
FEATURES
source.

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Best Local Similarity 96.3%; Pred. No. 2.6;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTGTTAAGCCGGCCG 27
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516 CCTATCCTGTTTGTGTTAAGCCGGCCG 542

Search completed: April 9, 2006, 07:14:32

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 05:55:33 ; Search time 381.134 Seconds
(without alignments)
472.135 Million cell updates/sec

Title: US-10-661-094-1_COPY_870_896
Perfect score: 27
Sequence: 1 cctatccgttttctgtaagccgagcgc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Listing first 120 summaries

Database :

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1: geneseqn1980s: *
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12: geneseqn2004as: *
13: geneseqn2004bs: *
14: geneseqn2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	27	100.0	1218	4	AAH01064 Enterococ
5	27	100.0	1232	4	AAH01063 Enterococ
6	27	100.0	1237	4	AAH01061 Enterococ
7	27	100.0	1241	4	AAH01058 Enterococ
8	27	100.0	1249	4	AAH01059 Enterococ
9	27	100.0	1263	4	AAH01062 Enterococ
10	27	100.0	1265	4	AAH01065 Enterococ
11	27	100.0	1265	4	AAH01066 Enterococ
12	27	100.0	1272	4	AAH01060 Enterococ
13	27	100.0	1768	4	AAH01148 Enterococ
14	27	100.0	1768	12	AD047257 B. faeciu
15	27	100.0	1768	14	ADY59927 Enterococ
16	27	100.0	2607	2	AAH01150 Enterococ
17	27	100.0	3946	4	AAH01150 Enterococ
18	27	100.0	7227	2	AAQ25183 E. faecium
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23	20.8	77.0	110000	2	AAQ20248	07
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30	20.6	76.3	556	12	AD047259	Enterococ
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35	20.6	76.3	801	14	ADY59937	Enterococ
36	20.6	76.3	801	14	ADY59940	Enterococ
37	20.6	76.3	801	14	ADY59943	Enterococ
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40	20.6	76.3	801	14	ADY59938	Enterococ
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49	20.6	76.3	1141	2	AAQ69235	Enterococ
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55	19.6	72.6	1191	8	ACA52513	Prokaryot
56	19.6	72.6	21170	2	AAQ20535	Polynucle
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64	18.2	67.4	819	13	ADT48822	Enterococ
65	18.2	67.4	1473	13	ADT42360	Enterococ
66	18.2	67.4	95109	6	ABQ96654	Human mem
67	18.2	67.4	1206	8	ACA45223	Prokaryot
68	18	66.7	6378	12	ADQ21325	Human sof
69	18	66.7	6502	13	ACN43122	Human sof
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77	17.8	65.9	2013	13	ADU00970	Human encod
78	17.8	65.9	88208	14	ADZ13389	Human can
79	17.8	65.9	88445	13	ABD33536	Human can
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81	17.8	65.9	121434	14	AEA08528	Human Not
82	17.8	65.9	251	12	ADQ06952	Human Not
83	17.6	65.2	255	12	ADQ06944	Human Not
84	17.6	65.2	263	12	ADQ06946	Human Not
85	17.6	65.2	263	12	ADQ06946	Human Not
86	17.6	65.2	268	12	ADQ06945	Human Not
87	17.6	65.2	273	12	ADQ06945	Human Not
88	17.6	65.2	277	5	ABV16923	Human pro
89	17.6	65.2	290	5	ABV16923	Human pro
90	17.6	65.2	430	5	ABV16923	Human pro
91	17.6	65.2	525	11	ACH96095	Human pro
92	17.6	65.2	943	13	ADX11876	Plant ful

93	17.6	65.2	1026	4	AAS53038	Aas53038 Enterococ
94	17.6	65.2	4948	2	AAT42134	Aat42134 I2C-1 gen
95	17.6	65.2	39982	8	AAD48290	Aad48290 Human enz
96	17.6	65.2	66685	4	AAS07380	Aas07380 Human gen
97	17.6	65.2	66686	6	AB573149	AB573149 Human CLA
98	17.4	64.4	318	10	ACF68191	ACF68191 Photorhab
99	17.4	64.4	486	4	AAH34587	Aah34587 Human col
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101	17.4	64.4	1053	12	AD062241	Ado62241 Transcrip
102	17.4	64.4	1053	11	ABD12733	Abd12733 Pseudomon
103	17.4	64.4	1262	13	ADX60508	Adx60508 Plant ful
104	17.4	64.4	1262	12	AD063288	Ado63288 Transcrip
105	17.4	64.4	1310	12	AD062242	Ado62242 Transcrip
106	17.4	64.4	1353	13	ADX53082	Adx53082 Plant ful
107	17.4	64.4	1512	11	ABD12707	Abd12707 Pseudomon
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109	17.4	64.4	2334	11	ABD12689	Abd12689 Pseudomon
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111	17.4	64.4	4081	2	AAV06585	AAV06585 Arbidlops
112	17.4	64.4	23070	9	ADA02507	Ada02507 Mouse Wnt
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114	17.4	64.4	23070	10	AD895755	Ad895755 Mouse Wnt
115	17.4	64.4	23982	14	AD212503	Ad212503 Murine ca
116	17.4	64.4	73882	13	AD873531	Ad873531 tcp gene
117	17.4	64.4	110000	10	ACF67367_09	Continuation (4 of
118	17.4	64.4	110000	10	ACF65384_3	Continuation (10 of
119	17.4	64.4	111836	13	ABD33102	Abd33102 Murine ca
120	17.4	64.4	256525	11	ACM44148	ACM44148 Mouse gen

ALIGNMENTS

RESULT 1

ADY59929 standard; DNA, 27 BP.

ID ADY59929 standard; DNA, 27 BP.

AC ADY59929; (first entry)

DT 02-JUN-2005 (first entry)

DE Enterococcus faecium vana probe SEQ ID NO:3.

XX DNA detection; antibiotic-resistance; vancomycin; vana; probe; ss.

XX Enterococcus faecium.

XX Synthetic.

XX US2005058985-A1.

XX 17-MAR-2005.

XX 12-SEP-2003; 2003US-00661094.

XX 12-SEP-2003; 2003US-00661094.

XX (DODG/) DODGSON K J.

XX Dodgson KJ;

XX WPI; 2005-222218/23.

XX Detecting vana and/or vana nucleic acid molecules in a sample, useful for

XX e.g. identifying vancomycin-resistant enterococcus, comprises using vana-

XX and/or vana-specific oligonucleotide probes or primers.

XX Claim 34; SEQ ID NO 3; 33pp; English.

XX The invention relates to a method for detecting vancomycin resistance

XX gene vana and/or vana nucleic acid molecules in a sample comprising

XX contacting the sample with a vana- and/or vana-specific oligonucleotide

XX probe or primer, and detecting or determining the presence or amount of

XX hybrid formation or amplified nucleic acid. Also described: (1) an

CC oligonucleotide composition comprising a first oligonucleotide comprising
 CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
 CC 898-917 of the vana gene, or its complement or portion, or an
 CC oligonucleotide comprising sequences substantially corresponding to
 CC nucleotides 387-404, 406-423 or 425-446 of the vana gene, or its
 CC complement or portion, where the oligonucleotide hybridizes under
 CC stringent hybridization conditions to vana or vana DNA; and (2) a kit
 CC comprising one or more oligonucleotide(s) specific for a vana gene and/or
 CC vana gene in a test sample, comprising the oligonucleotide mentioned
 CC above. The method and kit are useful for detecting and/or amplifying
 CC genes (i.e. vana and/or vana genes) in a test sample, or for identifying
 CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus);
 CC They may also be used in other industrial purposes, such as for quality
 CC control of food, water, pharmaceutical products or other products
 CC requiring microbiological control. The present sequence represents a
 CC probe for Enterococcus faecium vana, which is used in an example from the
 CC present invention.

XX Sequence 27 BP; 3 A; 8 C; 6 G; 10 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 27; DB 14; Length 27;

XX Best Local Similarity 100.0%; Pred. No. 0.018; Mismatches 0; Gaps 0;

XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 CCTATCCTGTTTGTGTTAAGCCGCGCC 27

XX 1 CCTATCCTGTTTGTGTTAAGCCGCGCC 27

XX RESULT 2

XX AAH02300 standard; DNA, 1032 BP.

XX ID AAH02300;

XX 24-JUL-2001 (first entry)

XX Enterococcus faecium nucleotide sequence SEQ ID NO:2293.

XX Species specific; genus specific; family specific; probe; detection;

XX identification; algal; archaeal; bacterial; fungal; parasitic;

XX microorganism; diagnosis; translation elongation factor Tu; toxin;

XX translation elongation factor G; RecA recombinase; resistance;

XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;

XX primer; ds.

XX Enterococcus faecium.

XX WO200123604-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000MO-CA001150.

XX 28-SEP-1999; 99CA-02283458.

XX 19-MAY-2000; 2000CA-02307010.

XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M,

XX Picard FJ, Roy PH;

XX WPI; 2001-245006/25.

XX Nucleic acid sequences are used to generate universal probes and primers

XX which can be used to identify and detect the presence of algal, archaeal,

XX bacterial, fungal and parasitic species in a test sample.

XX Disclosure; Page 1578; 1580pp; English.

XX The present invention describes a method for generating a repository of

XX nucleic acids of tuf, fup, atpD and/or recA genes from which probes

XX and/or primers are derived. The method comprises amplifying the nucleic

CC acids of determined algal, archaeal, bacterial, fungal and parasitological
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites; for universal detection and for specific and ubiquitous
 CC detection and identification of an algal, archaeal, bacterial, fungal and
 CC parasitological species, genus, family and group. A nucleic acid (1) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
 CC at least one antimicrobial agent resistance gene or at least one toxin
 CC gene. hexa nucleic acids are used for the specific and ubiquitous
 CC detection and for identification of *Streptococcus pneumoniae*. (1) can be
 CC used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
 CC *Corynebacterium* sp., *Enterobacteriaceae* group, *Bacterichia coli*,
 CC *Mycobacteriaceae* family, *Pseudomonas* group, *Streptococcus* sp., *Naissaria*
 CC *gonorrhoeae* and *Staphylococcus* sp. . Using DNA based tests provides faster
 CC results than substrate specificity tests as results can be determined in
 CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention

CC Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1032;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 CCTATCCTGTTTGTAAAGCGGCGC 27
 DB 494 CCTATCCTGTTTGTAAAGCGGCGC 520

RESULT 3

AAAF76039
 ID AAAF76039 standard; DNA; 1032 BP.

AC AAAF76039;

DT 22-MAY-2001 (first entry)

DE *Enterococcus faecium* vanA gene, SEQ ID NO:21.

CC Vancomycin resistance reduction; antisense expression inhibition;
 CC competitive inducer sequestration; vanH promoter; vanH gene product;
 CC *Enterococcus*; *Staphylococcus*; *Streptococcus*; Gram-positive bacterium;
 CC antibiotic susceptibility; ex vivo eradication; in vivo eradication;
 CC glycopeptide resistance; VanA gene cluster; ds.

OS *Enterococcus faecium*.

PN WO200112803-A2.

PD 22-FEB-2001.

PF 11-AUG-2000; 2000WO-US022086.

PR 17-AUG-1999; 99US-0149313P.

PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

PI Inouye RT, Torres-Viera C, Moellering R, Gold H, Eliopoulos GM;

DR WPI, 2001-211216/21.

CC Reducing vancomycin-resistance in vancomycin-resistant organism by
 CC introducing a antisense vancomycin-resistance molecule to inhibit
 CC vancomycin-resistance gene expression, or by enhancing vanH promoter
 CC expression.

Example: Page 52; 59pp; English.

CC The invention relates to methods of reducing vancomycin resistance in a
 CC vancomycin-resistant organism. One method involves introducing a
 CC vancomycin resistance gene antisense nucleic acid into the organism;
 CC antisense oligonucleotides complementary to AA76023-AA76031 are
 CC particularly preferred for this purpose. The second method involves
 CC providing additional vanH promoter sequences which are not operatively
 CC coupled to a vancomycin resistance gene, so that the phosphorylated vanH
 CC gene product (which induces vanH promoter activity) is competitively
 CC sequestered. Both methods are able to restore antibiotic susceptibility
 CC in glycopeptide resistant enterococci. The methods of the invention are
 CC useful for reducing vancomycin resistance in a vancomycin resistant
 CC organism, particularly *Enterococcus faecium* and *Enterococcus faecalis*,
 CC but also in other Gram-positive bacteria such as *Staphylococcus* sp. and
 CC *Streptococcus* sp., to which *Enterococcus faecium* and *Enterococcus*
 CC faecalis have the potential to transfer resistance determinants. The
 CC antisense molecules are useful in the treatment of infection and
 CC colonisation by vancomycin resistant enterococci and other clinically
 CC significant pathogens, and may be used for the ex vivo eradication of
 CC vancomycin-resistant enterococci from frequently colonised settings, such
 CC as intensive care units, haemodialysis units, and chronic care facilities
 CC ; for the in vivo clearance of vancomycin-resistant enterococci from
 CC colonised gastrointestinal or genitourinary tracts of animals, including
 CC humans; and in primary or adjuvant therapy for vancomycin-resistant
 CC enterococcal infections. The gene based strategy targets key vancomycin
 CC resistance determinants and results in restoration of vancomycin
 CC susceptibility in previously glycopeptide-resistant enterococci.
 CC Sequences AA76036-AA76042 represent genes of the *Enterococcus faecium*
 CC VanA gene cluster

CC Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1032;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 CCTATCCTGTTTGTAAAGCGGCGC 27
 DB 494 CCTATCCTGTTTGTAAAGCGGCGC 520

RESULT 4

AAH01064
 ID AAH01064 standard; DNA; 1218 BP.

AC AAH01064;

DT 24-JUL-2001 (first entry)

DE *Enterococcus gallinarum* nucleotide sequence SEQ ID NO:1055.

CC Species specific; genus specific; family specific; probe; detection;
 CC identification; algal, archaeal, bacterial, fungal, parasitological;
 CC microorganism; diagnosis; translation elongation factor Tu; toxin;
 CC translation elongation factor G; RecA recombinase; resistance;
 CC catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 CC primer; ds.

OS *Enterococcus gallinarum*.

PN WO200123604-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000WO-CA001150.

PR 28-SEP-1999; 99CA-02283458.

PA 19-MAY-2000; 2000CA-02307010.

PI (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

CC Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
 CC Plcard FJ, Roy PH;

DR WPI; 2001-245006/25.

XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitological species in a test sample.

PS Claim 27; Page 1001:1002; 1580bp; English.

XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Baccherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

SQ Sequence 1218 BP; 364 A; 226 C; 311 G; 317 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1218;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCGCGGC 27

DB 568 CCTATCCTGTTTGTGTAAGCGCGGC 594

RESULT 5

AAH01063

ID AAH01063 standard; DNA; 1232 BP.

XX AAH01063;

DT 24-JUL-2001 (first entry)

DE Enterococcus faecalis nucleotide sequence SEQ ID NO:1054.

XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitological;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; de.

OS Enterococcus faecalis.

XX MO200123604-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-CA001150.

XX 28-SEP-1999; 99CA-02283458.

XX 19-MAY-2000; 2000CA-02307010.

PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

PI Picard FU, Roy PH;

XX WPI; 2001-245006/25.

XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitological species in a test sample.

PS Claim 27; Page 1001; 1580bp; English.

XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Baccherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

SQ Sequence 1232 BP; 367 A; 228 C; 313 G; 323 T; 0 U; 1 Other;

Query Match 100.0%; Score 27; DB 4; Length 1232;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCGCGGC 27

DB 578 CCTATCCTGTTTGTGTAAGCGCGGC 604

RESULT 6

AAH01061

ID AAH01061 standard; DNA; 1237 BP.

XX AAH01061;

DT 24-JUL-2001 (first entry)

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1052.

XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitological;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; de.

OS Enterococcus faecium.

XX MO200123604-A2.

XX 05-APR-2001.

PF 28-SEP-2000; 2000MO-CA001150.
XX
XX 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX WPI; 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitological species in a test sample.
XX
XX Claim 27; Page 999; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection of
CC any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
CC
SQ Sequence 1237 BP; 366 A; 235 C; 314 G; 322 T; 0 U; 0 Other;
Query Match 100.0%; Score 27; DB 4; Length 1237;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTATCGTGTGTTGTTAGCGCGC 27
DB 590 CCTATCGTGTGTTGTTAGCGCGC 616
RESULT 7
AAH01058
ID AAH01058 standard; DNA; 1241 BP.
XX
XX AAH01058;
XX
XX 24-JUL-2001 (first entry)
XX
XX Enterococcus faecium nucleotide sequence SEQ ID NO:1049.
XX
XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitological;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; ds.
XX
XX Enterococcus faecium.
OS

XX
XX W0200123604-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000MO-CA001150.
XX
XX 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX WPI; 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitological species in a test sample.
XX
XX Claim 27; Page 997; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection of
CC any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
CC
SQ Sequence 1241 BP; 371 A; 228 C; 317 G; 325 T; 0 U; 0 Other;
Query Match 100.0%; Score 27; DB 4; Length 1241;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTATCGTGTGTTGTTAGCGCGC 27
DB 561 CCTATCGTGTGTTGTTAGCGCGC 587
RESULT 8
AAH01059
ID AAH01059 standard; DNA; 1249 BP.
XX
XX AAH01059;
XX
XX 24-JUL-2001 (first entry)
XX
XX Enterococcus gallinarum nucleotide sequence SEQ ID NO:1050.
XX
XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitological;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX

KW translation elongation factor G, RecA recombinase, resistance;
KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; ds.
OS Enterococcus gallinarum.
XX WO200123604-A2.
XX 05-APR-2001.
XX 28-SEP-2000; 2000WO-CA001150.
XX 28-SEP-1999; 99CA-02283458.
XX 19-MAY-2000; 2000CA-02307010.
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
XX Picard FJ, Roy PH;
XX WPI; 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
XX Claim 27; Page 998; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and for identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
XX Sequence 1249 BP; 373 A; 235 C; 316 G; 325 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 27; DB 4; Length 1249;
XX Best Local Similarity 100.0%; Pred. No. 0.031;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CCGATCTGTTTGTGTTAAGCCGCGC 27
Db 590 CCGATCTGTTTGTGTTAAGCCGCGC 616
XX
XX RESULT 9
XX AAH01062
XX ID AAH01062 standard; DNA; 1263 BP.
XX
XX AAH01062;
XX
XX 24-JUL-2001 (first entry)
XX

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1053.
XX
XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitical;
XX microorganisms; diagnosis; translation elongation factor Tuf toxin;
XX translation elongation factor G, RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; ds.
XX Enterococcus faecium.
XX WO200123604-A2.
XX 05-APR-2001.
XX 28-SEP-2000; 2000WO-CA001150.
XX 28-SEP-1999; 99CA-02283458.
XX 19-MAY-2000; 2000CA-02307010.
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
XX Picard FJ, Roy PH;
XX WPI; 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
XX Claim 27; Page 1000; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and for identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
XX Sequence 1263 BP; 378 A; 234 C; 321 G; 330 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 27; DB 4; Length 1263;
XX Best Local Similarity 100.0%; Pred. No. 0.031;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CCGATCTGTTTGTGTTAAGCCGCGC 27
Db 582 CCGATCTGTTTGTGTTAAGCCGCGC 608
XX
XX RESULT 10
XX AAH01065
XX ID AAH01065 standard; DNA; 1265 BP.
XX

XX AAH01065;
AC 24-JUL-2001 (first entry)
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1056.
XX
XX Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitica;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
OS Enterococcus faecium.
PN WO200123604-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000MO-CA001150.
XX
XX 28-SEP-1999; 99CA-02283458.
XX 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
XX WPI; 2001-24506/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitica species in a test sample.
XX
XX
XX Claim 27; Page 1002; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitica
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitica species, genus, family and group. A nucleic acid (1) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (1) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacans, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
XX Sequence 1265 BP; 379 A; 237 C; 320 G; 329 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 27; DB 4; Length 1265;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
AAH01066 standard; DNA; 1269 BP.
ID AAH01066;
XX
XX 24-JUL-2001 (first entry)
XX
XX Enterococcus faecium nucleotide sequence SEQ ID NO:1057.
DE
XX Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitica;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
OS Enterococcus faecium.
PN WO200123604-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000MO-CA001150.
XX
XX 28-SEP-1999; 99CA-02283458.
XX 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
XX WPI; 2001-24506/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitica species in a test sample.
XX
XX
XX Claim 27; Page 1003; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitica
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitica species, genus, family and group. A nucleic acid (1) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (1) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacans, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
XX Sequence 1269 BP; 380 A; 238 C; 321 G; 330 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 27; DB 4; Length 1269;
Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTAAAGCCGCGC 27
 Db 590 CCTATCCTGTTTGTAAAGCCGCGC 616

RESULT 12
 AAH01060
 ID AAH01060 standard; DNA; 1272 BP.

AC AAH01060;

DT 24-JUL-2001 (first entry)

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1051.

KM Species specific; genus specific; family specific; probe; detection;
 KM identification; algal; archaeal; bacterial; fungal; parasitica;
 KM microorganism; diagnosis; translation elongation factor Tu; toxin;
 KM translation elongation factor G; RecA recombinase; resistance;
 KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KM primer; ds.

OS Enterococcus faecium.

PN WO200123604-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000MO-CA001150.

PR 28-SEP-1999; 99CA-02283458.

PR 19-MAY-2000; 2000CA-02307010.

PA (INFR-) INFECTIO DIAGNOSTIC (IDI) INC.

PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

PI Picard FJ, Roy PH;

DR WPI; 2001-245006/25.

PT Nucleic acid sequences are used to generate universal probes and primers
 PT which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitica species in a test sample.

PS Claim 27; Page 998-999; 1580pp; English.

XX The present invention describes a method for generating a repository of
 CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitica
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and identification of an algal, archaeal, bacterial, fungal and
 CC parasitica species, genus, family and group. A nucleic acid (I) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
 CC at least one antimicrobial agent resistance gene or at least one toxin
 CC gene. hexA nucleic acids are used for the specific and ubiquitous
 CC detection and for identification of Streptococcus pneumoniae. (I) can be
 CC used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
 CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
 CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
 CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 CC results than substrate specificity tests as results can be determined in
 CC an hour and improved accuracy is also achieved. AAH0010 to AAH002304
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention

XX SQ Sequence 1272 BP; 379 A; 232 C; 325 G; 336 T; 0 U; 0 Other;
 Query Match 100.0%; Score 27; DB 4; Length 1272;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTAAAGCCGCGC 27
 Db 570 CCTATCCTGTTTGTAAAGCCGCGC 596

RESULT 13
 AAH01148
 ID AAH01148 standard; DNA; 1768 BP.

AC AAH01148;

DT 24-JUL-2001 (first entry)

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1139.

KM Species specific; genus specific; family specific; probe; detection;
 KM identification; algal; archaeal; bacterial; fungal; parasitica;
 KM microorganism; diagnosis; translation elongation factor Tu; toxin;
 KM translation elongation factor G; RecA recombinase; resistance;
 KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KM primer; ds.

OS Enterococcus faecium.

PN WO200123604-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000MO-CA001150.

PR 28-SEP-1999; 99CA-02283458.

PR 19-MAY-2000; 2000CA-02307010.

PA (INFR-) INFECTIO DIAGNOSTIC (IDI) INC.

PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

PI Picard FJ, Roy PH;

DR WPI; 2001-245006/25.

PT Nucleic acid sequences are used to generate universal probes and primers
 PT which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitica species in a test sample.

PS Disclosure; Page 1033-1034; 1580pp; English.

XX The present invention describes a method for generating a repository of
 CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitica
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and identification of an algal, archaeal, bacterial, fungal and
 CC parasitica species, genus, family and group. A nucleic acid (I) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
 CC at least one antimicrobial agent resistance gene or at least one toxin
 CC gene. hexA nucleic acids are used for the specific and ubiquitous
 CC detection and for identification of Streptococcus pneumoniae. (I) can be
 CC used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adiacens, Bordetella coli,
 CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
 CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria

CC gonorrhoeae and *Staphylococcus* sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AH00010 to AH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

XX Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

SO Query Match 100.0%; Score 27; DB 4; Length 1768;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTTAAGCGGCGC 27

DB 870 CCTATCCTGTTTGTGTTAAGCGGCGC 896

RESULT 14

ADO47257 ADO47257 standard; DNA; 1768 BP.

AC ADO47257;

XX 15-JUL-2004 (first entry)

DE E. faecium vancomycin resistance gene, vanA.

XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanA;

KM gene; ds; hospital acquired infection; VRE;

XX fluorescence resonance energy transfer; FRET.

OS Enterococcus faecium.

XX US200405836-A1.

XX 25-MAR-2004.

PF 25-SEP-2002; 2002US-00254260.

XX 25-SEP-2002; 2002US-00254260.

PA (COCK)/ COCKERILL F R.

XX (SLOAN)/ SLOAN L M.

PI Cockerill FR, Sloan LM;

XX WPI; 2004-268785/25.

PT Detecting presence or absence of vancomycin-resistant enterococci in

XX biological sample from individual comprises using real time polymerase

PT chain reaction.

XX Disclosure; SEQ ID NO 10; 23pp; English.

CC The invention relates to detecting the presence or absence of vancomycin-

CC resistant enterococci (VRE) in a sample, comprising performing a cycling

CC step by amplifying a sample with pair of vanA or vanB primers and

CC hybridising the sample with a pair of vanA or vanB probes, labelled with

CC donor and acceptor fluorescent group, respectively, detecting

CC fluorescence resonance energy transfer (FRET), where the presence of FRET

CC indicates presence of VRE. Also included is an article of manufacture,

CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes

CC and a donor fluorescent group and a corresponding fluorescent group. The

CC method is useful for detecting the presence or absence of vancomycin-

CC resistant enterococci in a biological sample, e.g. stool samples, anal or

CC perirectal swabs, blood and body fluids from an individual. The method

CC replaces standard culture methods and reduces the cost. The method

CC provides rapid vancomycin resistant enterococcus real time PCR assay

CC which is useful for beginning the antimicrobial therapy immediately to

CC treat hospital acquired infection. The present sequence is an

CC enterococcal vanA, vancomycin resistance gene.

XX Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 27; DB 12; Length 1768;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTTAAGCGGCGC 27

DB 870 CCTATCCTGTTTGTGTTAAGCGGCGC 896

RESULT 15

ADY59927 ADY59927 standard; DNA; 1768 BP.

AC ADY59927;

XX 02-JUN-2005 (first entry)

DE Enterococcus faecium vanA DNA sequence SEQ ID NO:1.

XX DNA detection; antibiotic-resistance; vancomycin; vanA; gene; ds.

OS Enterococcus faecium.

XX US2005058985-A1.

XX 17-MAR-2005.

PF 12-SEP-2003; 2003US-00661094.

XX 12-SEP-2003; 2003US-00661094.

PA (DODG)/ DODGSON K J.

XX Dodgson KJ;

XX WPI; 2005-222218/23.

PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for

XX e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-

XX and/or vanB-specific oligonucleotide probes or primers.

XX Example 1; SEQ ID NO 1; 33pp; English.

CC The invention relates to a method for detecting vancomycin resistance

CC gene vanA and/or vanB nucleic acid molecules in a sample comprising

CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide

CC probe or primer, and detecting or determining the presence or amount of

CC hybrid formation or amplified nucleic acid. Also described: (1) an

CC oligonucleotide composition comprising a first oligonucleotide comprising

CC sequences substantially corresponding to nucleotides 870-896, 851-868 or

CC 898-917 of the vanA gene, or its complement or portion, or an

CC oligonucleotide comprising sequences substantially corresponding to

CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its

CC complement or portion, where the oligonucleotide hybridises under

CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit

CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or

CC vanB gene in a test sample, comprising the oligonucleotide mentioned

CC above. The method and kit are useful for detecting and/or amplifying

CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying

CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).

CC They may also be used in other industrial purposes, such as for quality

CC control of food, water, pharmaceutical products or other products

CC requiring microbiological control. The present sequence represents an

CC Enterococcus faecium vanA nucleotide sequence from the present invention.

XX Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 27; DB 14; Length 1768;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTTAAGCGGCGC 27

Db 870 CCTATCCTGTTTGTGTAAGCCGCGC 896

RESULT 16

AAT28569 ID AAT28569 standard; DNA; 2607 BP.

XX AAT28569;

DT 01-APR-1997 (first entry)

XX Bacterial antibiotic resistance gene, vanH, vanA and vanX, probe.

DE Detection; probe; amplification primer; bacterial pathogen; pneumonia;
KM Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
KM Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
KM Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;
KM Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
KM Haemophilus influenzae; Moraxella catarrhalis; septicemia; meningitis;
KM infection; intra-abdominal infection; skin infection;
KM bacterial resistance; beta-lactam antibiotic; ds.

XX Synthetic.

PN MO9608582-A2.

PD 21-MAR-1996.

PF 12-SEP-1995; 95MO-CA000528.

PR 12-SEP-1994; 94US-00304732.

XX (BERG/) BERGERON M. G.
PA (OUEL/) OUELLETTE M.
PA (ROY/) ROY P H.

PI Bergeron MG, Ouellette M, Roy PH;

DR WPI; 1996-179953/18.

PT Method for the detection of bacterial species using probes and primers -
PT allows detection and quantification of antibiotic resistant bacteria in
PT patients, the environment and food.

XX Claim 94; Page 145-147; 216pp; English.

CC The sequences given in AAT28560-76 represent fragments derived from
CC bacterial antibiotic resistance genes which were used as probes in the
CC method of the invention for the detection of bacterial species in a
CC sample. The method of the invention comprises using probes and/or
CC amplification primers which are specific, ubiquitous and sensitive for
CC determining the presence and/or amount of nucleic acids from selected
CC bacterial species in any sample, where the bacterial nucleic acid
CC comprises a selected target region hybridisable with the probes or
CC primers. The method comprises contacting the sample with the probes or
CC primers and detecting the presence and/or amount of hybridised primers or
CC amplification products as an indication of the presence and/or amount of
CC the bacterial species. This method may be used to detect commonly
CC encountered bacterial pathogens, e.g. Escherichia coli, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus
CC Enterococcus faecalis, Staphylococcus saprophyticus, Streptococcus
CC pyogenes, Haemophilus influenzae and Moraxella catarrhalis. These
CC bacterial species are associated with approx. 90% of urinary tract
CC infections and with a high percentage of other severe infections
CC including septicemia, meningitis, pneumonia, intra-abdominal infections,
CC skin infections and other severe respiratory tract infections. The method
CC may also be used to evaluate a bacterial resistance to beta-lactam
CC antibiotics

SQ Sequence 2607 BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 2; Length 2607;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27

Db 1455 CCTATCCTGTTTGTGTAAGCCGCGC 1481

RESULT 17

ABA76994 ID ABA76994 standard; DNA; 2607 BP.

XX ABA76994;

DT 28-JAN-2002 (first entry)

XX Antibiotic resistance detection polynucleotide SEQ ID NO 170.

DE Detection; bacterial species; animal; food; environment;
KM antibiotic resistance; ds.

XX Unidentified.

PN NZ501596-A.

PD 29-JUN-2001.

PF 12-SEP-1995; 95NZ-00501596.

PR 12-SEP-1995; 95NZ-00501596.

PA (IDI-) IDI INFECTION DIAGNOSTIC INC.

PI Bergeron MG, Ouellette M, Roy PH;

DR WPI; 2001-615034/71.

PT Method for detecting target bacterial species in a sample, comprises
PT detecting the presence or amount of bacterial nucleic acid amplified by a
PT primer derived from bacterial DNA, specific for the target bacterial
PT species.

XX Claim 16; Page 160-162; 168pp; English.

CC The invention relates to detecting target bacterial species suspected to
CC be present in a sample, comprising contacting nucleic acids of target
CC bacterial species with an amplification primer pair derived from a
CC bacterial DNA fragment (ABA76825-ABA76861) specific for the target
CC bacterial species but ubiquitous for different strains, amplifying the
CC nucleic acid and detecting the presence or amount of an amplified
CC sequence as an indication of the presence or amount of the target
CC bacterial species. The invention includes primers and probes (ABA76862-
CC ABA76984) against the target bacterial species, especially E. coli,
CC K. pneumoniae, P. aeruginosa, P. mirabilis, S. pneumoniae, S. aureus,
CC M. catarrhalis and/or group A Streptococci producing exotoxin A gene spe
CC A, suspected to be present in a sample which is obtained from human
CC patients, animals, environment or food, and which consists of one or more
CC bacterial colonies. Oligonucleotide probes and primers complementary to
CC the bacterial genes encoding resistance to antibiotics such as bla(tem),
CC bla(rob), bla(shv), aacB, aacC1, aacC3, aacA4, mecA, vanA, vanH,
CC vanX, sacA, aacA-phd, vat, vga, mcrA, sul and/or int (ABA76985-ABA77001)
CC are also useful to identify commonly encountered and clinically important
CC resistance genes. The invention provides a rapid method of bacterial
CC identification that can be achieved, which reduces the time currently
CC required for the identification of pathogens in the clinical laboratory

SQ Sequence 2607 BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 2607;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCCGCGC 27
 DB 1455 CCTATCCTGTTTGTAAAGCCGCGC 1481

RESULT 18
 ID AAH01150 standard; DNA; 3946 BP.

AAH01150;

24-JUL-2001 (first entry)

Enterococcus faecium nucleotide sequence SEQ ID NO:1141.

Species specific; genus specific; family specific; probe; detection;
 identification; algal; archaeal; bacterial; fungal; parasitica;
 microorganism; diagnosis; translation elongation factor Tu; toxin;
 translation elongation factor G; RecA recombinase; resistance;
 catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 primer; ds.

Enterococcus faecium.

MO200123604-A2.

05-APR-2001.

28-SEP-2000; 2000WO-CA001150.

28-SEP-1999; 99CA-02283458.

19-MAY-2000; 2000CA-02307010.

(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

Bergeon MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

Picard FJ, Roy PH;

WPI; 2001-245006/25.

Nucleic acid sequences are used to generate universal probes and primers
 which can be used to identify and detect the presence of algal, archaeal,
 bacterial, fungal and parasitica species in a test sample.

Disclosure; Page 1035-1036; 1580pp; English.

The present invention describes a method for generating a repository of
 nucleic acids of tuf, fus, atpD and/or recA genes from which probes
 and/or primers are derived. The method comprises amplifying the nucleic
 acids of determined algal, archaeal, bacterial, fungal and parasitica
 species with a combination of defined primer pairs. The method can be
 used for producing probes and/or primers for detecting one or more
 related microorganisms e.g. algae, archaea, bacteria, fungi and
 parasites, for universal detection and for specific and ubiquitous
 detection and identification of an algal, archaeal, bacterial, fungal and
 parasitica species, genus, family and group. A nucleic acid (1) obtained
 using the method of the invention can be used for the universal detection
 of any bacterium, fungus or parasite in a sample and for the detection of
 at least one antimicrobial agent resistance gene or at least one toxin
 gene. hexa nucleic acids are used for the specific and ubiquitous
 detection and for identification of Streptococcus pneumoniae. (1) can be
 used to design a therapeutic agent which is effective against
 microorganisms. Microbial species or genus or family or phylum or group
 which can be detected include Abiotrophia adiacens, Bordetella sp.,
 Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
 Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
 gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 results than substrate specificity tests as results can be determined in
 an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 represent nucleotide sequences and primers/probes which are given in the
 exemplification of the present invention

Sequence 3946 BP; 1235 A; 706 C; 936 G; 1065 T; 0 U; 0 Other;
 Query Match 100.0%; Score 27; DB 4; Length 3946;
 Best Local Similarity 100.0%; Pred. No. 0.037;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCCGCGC 27
 DB 1455 CCTATCCTGTTTGTAAAGCCGCGC 1481

RESULT 19

AAQ25183

ID AAQ25183 standard; DNA; 7227 BP.

AAQ25183;

24-OCT-2003 (revised)

25-MAR-2003 (revised)

20-NOV-1992 (first entry)

E.faecium antibiotic resistance genes and flanking sequences.

Glycopeptide antibiotic; vancomycin; telicoplanin; resistant;

D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;

inverted repeats; vanR; vanS; vanH; vanA; vanX; se.

Enterococcus faecium; BM4147.

MO9207942-A1.

14-MAY-1992.

29-OCT-1991; 91WO-FR000855.

31-OCT-1990; 90FR-00013579.

(INSP) INST PASTEUR.

Arthur M, Dutka-Malen S, Molinas C, Courvalin P;

WPI; 1992-183677/22.

P-PSDB; AAR24305, AAR24306, AAR24307.

Polypeptides involved in expression of glycopeptide antibiotic resistance

- useful in diagnosing presence of Gram-positive enterococcal strains

e.g. Enterococcus faecium and E. Gallinarum.

Disclosure; Fig 4; 163pp; French.

This sequence contains the genes vanH, vanA, vanX, vanR and vanS. The
 proteins encoded by the latter two genes (i.e. proteins VanR and Vans)
 have a regulatory function and control expression of the other three
 ("protective") proteins. See also AAQ25179-025182. (Updated on 25-MAR-
 2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
 (Updated on 24-OCT-2003 to standardise OS field)

QY 1 CCTATCCTGTTTGTAAAGCCGCGC 27
 DB 5018 CCTATCCTGTTTGTAAAGCCGCGC 5044

RESULT 20
 AAQ25178
 ID AAQ25178 standard; DNA; 10851 BP.

AC AAQ25178;

XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 20-NOV-1992 (first entry)
XX E. faecium antibiotic resistance genes and Tn sequences.
DE
XX glycopeptide antibiotic; vancomycin; telicoplanin; resistant;
KM D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;
KM inverted repeats; ss.
XX Enterococcus faecium; BM4147.
XX
XX Key Location/Qualifiers
FH complement(1..3189)
FT CDS
FT /product= "transposase"
FT /note= "coded by the (-) strand - see AAQ25179"
FT repeat_unit
FT 1..38
FT /cag= j
FT /rpt_type= INVERTED
FT 3187..3762
FT /cag= b
FT /product= "resolvase"
FT 3976..4671
FT CDS
FT /cag= c
FT /product= "VanR"
FT /note= "VanR is a transcription activator"
FT 4649..5803
FT /cag= d
FT /product= "Vans"
FT /note= "Vans is a regulatory protein"
FT 6018..6986
FT /cag= e
FT /product= "VanH"
FT 6979..8010
FT /cag= f
FT /product= "Vana"
FT 8016..8624
FT CDS
FT /cag= g
FT /product= "VanX"
FT 9052..9963
FT /cag= h
FT /product= "Vany"
FT 10116..10601
FT /cag= i
FT /product= "Vanz"
FT repeat_unit
FT complement(10814..10851)
FT /cag= k
FT /rpt_type= INVERTED
XX
XX W09207942-A1.
XX
XX 14-MAY-1992.
XX
XX 29-OCT-1991; 91WO-FR000855.
XX
XX 31-OCT-1990; 90FR-00013579.
XX
XX (INSP) INST PASTEUR.
XX
XX Arthur M, Dukta-Malen S, Molinas C, Courvalin P;
XX
XX WPI; 1992-183677/22.
XX P-PSDB; AAR24294, AAR24295, AAR24296, AAR24297, AAR24298, AAR24299,
XX AAR24300, AAR24301, AAR24302.
XX
XX Polypeptides involved in expression of glycopeptide antibiotic resistance
PT - useful in diagnosing presence of Gram-positive enterococcal strains
PT e.g. Enterococcus faecium and E. Gallinarum.
XX
XX Claim 9; Fig 8; 163pp; French.
XX

CC This is a transposon sequence. The transposon comprises the genes
CC necessary for expression of resistance to glycopeptides in Enterococcus
CC faecium. It also contains genes associated with resistance, e.g. involved
CC in regulation of expression of the resistance genes or in the amount of
CC polypeptides produced. See also AAQ25179-Q25183. (Updated on 25-MAR-2003
CC to correct FN field.) (Updated on 25-MAR-2003 to correct FI field.)
CC (Updated on 24-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 10851 BP; 3399 A; 1960 C; 2234 G; 3258 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 27; DB 2; Length 10851;
XX Best Local Similarity 100.0%; Pred. No. 0.042;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CCTATCCTGTTTGTAAAGCCGCGCC 27
Db 7472 CCTATCCTGTTTGTAAAGCCGCGCC 7498
XX
XX RESULT 21
XX AAF76019
XX ID AAF76019 standard; DNA; 10851 BP.
XX
XX AAF76019;
XX
XX 22-MAY-2001 (first entry)
XX
XX E. faecium Vana vancomycin resistance gene cluster, SEQ ID NO:1.
XX
XX Vancomycin resistance reduction; antisense expression inhibition;
XX competitive inducer sequestration; vanH promoter; vanR gene product;
XX Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium;
XX antibiotic susceptibility; ex vivo eradication; in vivo eradication;
XX glycopeptide resistance; Vana gene cluster; de.
XX
XX Enterococcus faecium.
XX
XX W0200112803-A2.
XX
XX 22-FEB-2001.
XX
XX 11-AUG-2000; 2000MO-US022086.
XX
XX 17-AUG-1999; 99US-0149313P.
XX
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX Inouye RT, Torres-Viera C, Moellering R, Gold H, Eliopoulos GM;
XX WPI; 2001-211216/21.
XX
XX Reducing vancomycin-resistance in vancomycin-resistant organism by
XX introducing a antisense vancomycin-resistance molecule to inhibit
XX vancomycin-resistance gene expression, or by enhancing vanH promoter
XX expression.
XX
XX Claim 24; Page 41-44; 59pp; English.
XX
XX The invention relates to methods of reducing vancomycin resistance in a
XX vancomycin-resistant organism. One method involves introducing a
XX vancomycin resistance gene antisense nucleic acid into the organism;
XX antisense oligonucleotides complementary to AAF76023-AAF76031 are
XX particularly preferred for this purpose. The second method involves
XX providing additional vanH promoter sequences which are not operatively
XX coupled to a vancomycin resistance gene, so that the phosphorylated vanR
XX gene product (which induces vanH promoter activity) is competitively
XX sequestered. Both methods are able to restore antibiotic susceptibility
XX in glycopeptide resistant enterococci. The methods of the invention are
XX useful for reducing vancomycin resistance in a vancomycin resistant
XX organism, particularly Enterococcus faecium and Enterococcus faecalis,
XX but also in other Gram-positive bacteria such as Staphylococcus sp. and
XX Streptococcus sp., to which Enterococcus faecium and Enterococcus
XX faecalis have the potential to transfer resistance determinants. The

CC antisense molecules are useful in the treatment of infection and
CC colonisation by vancomycin resistant enterococci and other clinically
CC significant pathogens, and may be used for the ex vivo eradication of
CC vancomycin-resistant enterococci from frequently colonised settings, such
CC as intensive care units, haemodialysis units, and chronic care facilities
CC ; for the in vivo clearance of vancomycin-resistant enterococci from
CC colonised gastrointestinal or genitourinary tracts of animals, including
CC humans; and in primary or adjuvant therapy for vancomycin-resistant
CC enterococcal infections. The gene based strategy targets key vancomycin
CC resistance determinants and results in restoration of vancomycin
CC susceptibility in previously glycopeptide-resistant enterococci. The
CC present sequence represents the Enterococcus faecium Vana gene cluster
SQ Sequence 10851 BP; 3392 A; 1962 C; 2237 G; 3260 T; 0 U; 0 Other;
Query Match 100.0%; Score 27; DB 4; Length 10851;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCAATCCGTTTGTGTTAAGCCGCGC 27
Db 7472 CCAATCCGTTTGTGTTAAGCCGCGC 7498
RESULT 22
ACA22997
ID ACA22997 standard; DNA; 1071 BP.
AC ACA22997;
DT 19-JUN-2003 (first entry)
DE Prokaryotic essential gene #4654.
KM Antisense; de: prokaryotic essential gene; cell proliferation;
KM drug design; gene.
OS Borrelia burgdorferi.
XX WO200277183-A2.
XX 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KI, Zvekind JW,
XX Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
XX MPI: 2003-029926/02.
XX P-PSDB; ABU19127.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 10867; 1766bp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 1071 BP; 335 A; 127 C; 198 G; 411 T; 0 U; 0 Other;
Query Match 77.0%; Score 20.8; DB 8; Length 1071;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CTAATCCGTTTGTGTTAAGCCGCGC 25
Db 498 CTAATCCGTTTGTGTTAAGCCGCGC 521

RESULT 23
AAX20248_07
Continuation (8 of 10) of AAX20248 from base 700001 (Borrelia burgdorferi polynucleotide
WP Sequence split into 10 fragments LOCUS AAX20248 Accession Aax20248
WP Fragment Name Begin End
WP AAX20248_00 1 110000
WP AAX20248_01 100001 210000
WP AAX20248_02 200001 310000
WP AAX20248_03 300001 410000
WP AAX20248_04 400001 510000
WP AAX20248_05 500001 610000
WP AAX20248_06 600001 710000
WP AAX20248_07 700001 810000
WP AAX20248_08 800001 910000
WP AAX20248_09 900001 910715
Query Match 77.0%; Score 20.8; DB 2; Length 110000;
Best Local Similarity 91.7%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CTAATCCGTTTGTGTTAAGCCGCGC 25
Db 10177 CTAATCCGTTTGTGTTAAGCCGCGC 10200
RESULT 24
ADO47266/c
ID ADO47266 standard; DNA; 555 BP.
AC ADO47266;
XX
XX 15-JUL-2004 (first entry)
XX
XX Enterococcus vancomycin resistance gene, vanB ENEVANB2A.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
XX KW gene; de: hospital acquired infection; VRB;
XX fluorescence resonance energy transfer; FRST.

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XX OS Enterococcus sp.
XX PN US2004058336-A1.
XX PD 25-MAR-2004.
XX PF 25-SEP-2002; 2002US-00254260.
XX PR 25-SEP-2002; 2002US-00254260.
XX PA (COCK/) COCKERILL F R.
XX PI (SLOA/) SLOAN L M.
XX PT Cockerill FR, Sloan LM;
XX DR WPI; 2004-268785/25.
XX PT Detecting presence or absence of vancomycin-resistant enterococci in
XX PT biological sample from individual comprises using real time polymerase
XX PT chain reaction.
XX PS Disclosure; SEQ ID NO 20; 23bp; English.
XX CC The invention relates to detecting the presence or absence of vancomycin-
XX CC resistant enterococci (VRE) in a sample, comprising performing a cycling
XX CC step by amplifying a sample with pair of vanA or vanB primers and
XX CC hybridising the sample with a pair of vanA or vanB probes, labelled with
XX CC donor and acceptor fluorescent group, respectively, detecting
XX CC fluorescence resonance energy transfer (FRET), where the presence of FRET
XX CC indicates presence of VRE. Also included is an article of manufacture,
XX CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
XX CC and a donor fluorescent group and a corresponding fluorescent group. The
XX CC method is useful for detecting the presence or absence of vancomycin-
XX CC resistant enterococci in a biological sample, e.g. stool samples, anal or
XX CC perirectal swabs, blood and body fluids from an individual. The method
XX CC replaces standard culture methods and reduces the cost. The method
XX CC provides rapid vancomycin resistant enterococcus real time PCR assay
XX CC which is useful for beginning the antimicrobial therapy immediately to
XX CC treat hospital acquired infection. The present sequence is an
XX CC enterococcal vanB, vancomycin resistance gene.
XX SQ Sequence 555 BP; 132 A; 161 C; 115 G; 145 T; 0 U; 2 Other;
XX
XX Query Match 76.3%; Score 20.6; DB 12; Length 555;
XX Best Local Similarity 85.2%; Pred. No. 23;
XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
XX Db 391 CCTACCTGTCTTGTGAAGCCGCGAC 365
XX
XX RESULT 25
XX ADO47264/c
XX ID ADO47264 standard; DNA; 556 BP.
XX AC ADO47264;
XX DT 15-JUL-2004 (first entry)
XX DE Enterococcus vancomycin resistance gene, vanB ENEVANB.
XX KM Vancomycin resistant enterococcus; vancomycin resistance gene; vanB,
XX KM gene; ds; hospital acquired infection; VRE;
XX KM fluorescence resonance energy transfer; FRET.
XX OS Enterococcus sp.
XX PN US2004058336-A1.
XX PD 25-MAR-2004.

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XX PF 25-SEP-2002; 2002US-00254260.
XX XX 25-SEP-2002; 2002US-00254260.
XX XX (COCK/) COCKERILL F R.
XX PA (SLOA/) SLOAN L M.
XX PI Cockerill FR, Sloan LM;
XX XX WPI; 2004-268785/25.
XX XX
XX PT Detecting presence or absence of vancomycin-resistant enterococci in
XX PT biological sample from individual comprises using real time polymerase
XX PT chain reaction.
XX PS Disclosure; SEQ ID NO 18; 23bp; English.
XX CC The invention relates to detecting the presence or absence of vancomycin-
XX CC resistant enterococci (VRE) in a sample, comprising performing a cycling
XX CC step by amplifying a sample with pair of vanA or vanB primers and
XX CC hybridising the sample with a pair of vanA or vanB probes, labelled with
XX CC donor and acceptor fluorescent group, respectively, detecting
XX CC fluorescence resonance energy transfer (FRET), where the presence of FRET
XX CC indicates presence of VRE. Also included is an article of manufacture,
XX CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
XX CC and a donor fluorescent group and a corresponding fluorescent group. The
XX CC method is useful for detecting the presence or absence of vancomycin-
XX CC resistant enterococci in a biological sample, e.g. stool samples, anal or
XX CC perirectal swabs, blood and body fluids from an individual. The method
XX CC replaces standard culture methods and reduces the cost. The method
XX CC provides rapid vancomycin resistant enterococcus real time PCR assay
XX CC which is useful for beginning the antimicrobial therapy immediately to
XX CC treat hospital acquired infection. The present sequence is an
XX CC enterococcal vanB, vancomycin resistance gene.
XX SQ Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;
XX
XX Query Match 76.3%; Score 20.6; DB 12; Length 556;
XX Best Local Similarity 85.2%; Pred. No. 23;
XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
XX Db 392 CCTACCTGTCTTGTGAAGCCGCGAC 366
XX
XX RESULT 26
XX ADO47262/c
XX ID ADO47262 standard; DNA; 556 BP.
XX AC ADO47262;
XX DT 15-JUL-2004 (first entry)
XX DE E. faecalis vancomycin resistance gene, vanB EF94526.
XX KM Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
XX KM gene; ds; hospital acquired infection; VRE;
XX KM fluorescence resonance energy transfer; FRET.
XX OS Enterococcus faecalis.
XX PN US2004058336-A1.
XX PD 25-MAR-2004.
XX PF 25-SEP-2002; 2002US-00254260.
XX PR 25-SEP-2002; 2002US-00254260.
XX PA (COCK/) COCKERILL F R.
XX PA (SLOA/) SLOAN L M.
XX

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PI Cockerill FR, Sloan LM;
XX
XX WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 15; 23pp; English.
XX
XX The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanb or vanb primers and
CC hybridising the sample with a pair of vanb or vanb probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanb or vanb primers, a pair of vanb or vanb probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanb, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 133 A; 162 C; 116 G; 145 T; 0 U; 0 Other;
XX
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
Db 392 CCTACCGTGTCTTGTGAAGCGGCGC 366
XX
RESULT 27
AD047263/C
ID AD047263 standard; DNA; 556 BP.
XX
AC AD047263;
XX
DT 15-JUL-2004 (first entry)
XX
XX E. faecalis vancomycin resistance gene, vanb EFU94527.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanb;
XX gene; ds; hospital acquired infection; VRE;
XX fluorescence resonance energy transfer; FRET.
XX
XX Enterococcus faecalis.
XX
XX US2004058336-A1.
XX
XX 25-MAR-2004.
XX
XX 25-SEP-2002; 2002US-00254260.
XX
XX 25-SEP-2002; 2002US-00254260.
XX
XX (COCK/) COCKERILL F R.
XX (SLOA/) SLOAN L M.
XX
XX Cockerill FR, Sloan LM;
XX
XX WPI; 2004-268785/25.
XX
XX Detecting presence or absence of vancomycin-resistant enterococci in
XX biological sample from individual comprises using real time polymerase
XX chain reaction.
XX

XX
XX Disclosure; SEQ ID NO 17; 23pp; English.
XX
XX
XX The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanb or vanb primers and
CC hybridising the sample with a pair of vanb or vanb probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanb or vanb primers, a pair of vanb or vanb probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanb, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;
XX
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
Db 392 CCTACCGTGTCTTGTGAAGCGGCGC 366
XX
RESULT 28
AD047261/C
ID AD047261 standard; DNA; 556 BP.
XX
AC AD047261;
XX
DT 15-JUL-2004 (first entry)
XX
XX E. faecalis vancomycin resistance gene, vanb EFU94529.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanb;
XX gene; ds; hospital acquired infection; VRE;
XX fluorescence resonance energy transfer; FRET.
XX
XX Enterococcus faecalis.
XX
XX US2004058336-A1.
XX
XX 25-MAR-2004.
XX
XX 25-SEP-2002; 2002US-00254260.
XX
XX 25-SEP-2002; 2002US-00254260.
XX
XX (COCK/) COCKERILL F R.
XX (SLOA/) SLOAN L M.
XX
XX Cockerill FR, Sloan LM;
XX
XX WPI; 2004-268785/25.
XX
XX Detecting presence or absence of vancomycin-resistant enterococci in
XX biological sample from individual comprises using real time polymerase
XX chain reaction.
XX
XX Disclosure; SEQ ID NO 14; 23pp; English.
XX
XX The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanb or vanb primers and
CC hybridising the sample with a pair of vanb or vanb probes, labelled with
CC

CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
Db 392 CCTACCTGCTTGTGTAAGCCGCGC 366
RESULT 29
AD047265/c
ID AD047265 standard; DNA; 556 BP.
XX
AC AD047265;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU72704.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KM gene; ds; hospital acquired infection; VRE;
XX fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
XX (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
PS WPI; 2004-268785/25.
XX
DR
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 19; 23bp; English.
XX
XX The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.

CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 134 A; 158 C; 117 G; 147 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
Db 392 CCTACCTGCTTGTGTAAGCCGCGC 366
RESULT 30
AD047260/c
ID AD047260 standard; DNA; 556 BP.
XX
AC AD047260;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94528.
XX
KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KM gene; ds; hospital acquired infection; VRE;
XX fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
XX (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
PS WPI; 2004-268785/25.
XX
DR
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 13; 23bp; English.
XX
XX The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.

SQ Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 CCTATCCTGTTTGTGTAAGCCGGCGC 27
DB 392 CCTACCTGTCTTGTGTAAGCCGGCGC 366

RESULT 31
ADO47259/C
ID ADO47259 standard; DNA; 556 BP.
XX
XX ADO47259;
XX
XX 15-JUN-2004 (first entry)
XX
XX E. faecalis vancomycin resistance gene, vanB EFU94530.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
XX KM gene; ds; hospital acquired infection; VRB;
XX KM fluorescence resonance energy transfer; FRET.
XX
XX Enterococcus faecalis.
XX OS
XX US2004058336-A1.
XX PN
XX 25-MAR-2004.
XX PD
XX 25-SEP-2002; 2002US-00254260.
XX PF
XX 25-SEP-2002; 2002US-00254260.
XX PR
XX (COCK/) COCKERILL F R.
XX PA (SLOAN/) SLOAN L M.
XX PI
XX Cockerill FR, Sloan LM;
XX
XX WPI; 2004-268785/25.
XX DR
XX
XX Detecting presence or absence of vancomycin-resistant enterococci in
XX PT biological sample from individual comprises using real time polymerase
XX PT chain reaction.

PS Disclosure; SEQ ID NO 16; 23pp; English.
XX
XX The invention relates to detecting the presence or absence of vancomycin-
XX CC resistant enterococci (VRE) in a sample, comprising performing a cycling
XX CC step by amplifying a sample with pair of vanA or vanB primers and
XX CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
XX CC donor and acceptor fluorescent group, respectively, detecting
XX CC fluorescence resonance energy transfer (FRET), where the presence of FRET
XX CC indicates presence of VRE. Also included is an article of manufacture,
XX CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
XX CC and a donor fluorescent group and a corresponding fluorescent group. The
XX CC method is useful for detecting the presence or absence of vancomycin-
XX CC resistant enterococci in a biological sample, e.g. stool samples, anal or
XX CC perirectal swabs, blood and body fluids from an individual. The method
XX CC replaces standard culture methods and reduces the cost. The method
XX CC provides rapid vancomycin resistant enterococcus real time PCR assay
XX CC which is useful for beginning the antimicrobial therapy immediately to
XX CC treat hospital acquired infection. The present sequence is an
XX CC enterococcal vanB, vancomycin resistance gene.
XX
XX Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;
SQ

Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 CCTATCCTGTTTGTGTAAGCCGGCGC 27

DB 392 CCTACCTGTCTTGTGTAAGCCGGCGC 366

RESULT 32
AAO69230
ID AAO69230 standard; DNA; 589 BP.
XX
XX AAO69230;
XX
XX 25-MAR-2003 (revised)
XX DT 23-FEB-1995 (first entry)
XX
XX Enterococcus faecalis vanB gene (internal, amplified fragment).
XX DE
XX Gram positive bacteria; inducible glycopeptide resistance; vancomycin;
XX KM teicoplanin; antibiotic; vanB gene; ds.
XX
XX Enterococcus faecalis.
XX OS
XX
XX Key Location/Qualifiers
XX FH
XX misc_feature 2..589
XX FT /tag= a
XX FT /note= "amplified internal fragment of vanB gene"
XX
XX FR2699539-A1.
XX PN
XX 24-JUN-1994.
XX PD
XX 18-DEC-1992; 92FR-00015671.
XX PF
XX 18-DEC-1992; 92FR-00015671.
XX PR
XX (INSP) INST PASTEUR.
XX PA
XX Arthur M, Dutka-Malen S, Evers S, Courvalin P;
XX PT
XX WPI; 1994-227159/28.
XX DR
XX P-PSDB; AAR57150.
XX
XX New protein vanB involved in bacterial resistance to glyco-peptide(s) -
XX PT esp vancomycin, and related nucleic acid, vectors, transformed cells and
XX PT antibodies, for in vitro detection of resistant strains.
XX
XX Claim 8; Page 28; 39pp; French.
XX PS
XX The protein encoded by the vanB gene is implicated in resistance of Gram-
XX CC positive bacteria to glycopeptides, particularly to vancomycin. This
XX CC resistance is inducible by Vancomycin but not by teicoplanin. Sequence
XX CC AAO69230 is a claimed internal fragment of the vanB gene. (Updated on 25-
XX CC MAR-2003 to correct PN field.)
XX
XX Sequence 589 BP; 163 A; 124 C; 166 G; 136 T; 0 U; 0 Other;
SQ

Query Match 76.3%; Score 20.6; DB 2; Length 589;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 CCTATCCTGTTTGTGTAAGCCGGCGC 27
DB 165 CCTACCTGTCTTGTGTAAGCCGGCGC 191

RESULT 33
ADY59941
ID ADY59941 standard; DNA; 630 BP.
XX
XX ADY59941;
XX AC
XX 02-JUN-2005 (first entry)
XX DT
XX Enterococcus faecalis vanB DNA sequence SEQ ID NO:15.
XX DE

KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
 XX Enterococcus faecalis.
 XX US2005058985-A1.
 PN 17-MAR-2005.
 XX 12-SEP-2003; 2003US-00661094.
 XX 12-SEP-2003; 2003US-00661094.
 XX (DODG/) DODGSON K J.
 PA Dodgson KJ;
 PI WPI; 2005-222218/23.
 XX
 DR
 PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
 PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
 PT and/or vanB-specific oligonucleotide probes or primers.
 PS Example 1; SEQ ID NO 15; 33pp; English.
 XX
 CC The invention relates to a method for detecting vancomycin resistance
 CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
 CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
 CC probe or primer, and detecting or determining the presence or amount of
 CC hybrid formation or amplified nucleic acid. Also described: (1) an
 CC oligonucleotide composition comprising a first oligonucleotide comprising
 CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
 CC 898-917 of the vanA gene, or its complement or portion, or an
 CC oligonucleotide comprising sequences substantially corresponding to
 CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
 CC complement or portion, where the oligonucleotide hybridizes under
 CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
 CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
 CC vanB gene in a test sample, comprising the oligonucleotide mentioned
 CC above. The method and kit are useful for detecting and/or amplifying
 CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
 CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
 CC They may also be used in other industrial purposes, such as for quality
 CC control of food, water, pharmaceutical products or other products
 CC requiring microbiological control. The present sequence represents an
 CC Enterococcus faecalis vanB nucleotide sequence from the present
 CC invention.
 CC
 SQ Sequence 630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;
 Query Match 76.3%; Score 20.6; DB 14; Length 630;
 Best Local Similarity 85.2%; Pred. No. 24;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
 Db 185 CCTACCTGTTGTAAGCCGCGC 211
 RESULT 34
 ID ADY59942 standard; DNA; 783 BP.
 XX ADY59942;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Enterococcus faecalis vanB DNA sequence SEQ ID NO:16.
 XX
 KM DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
 XX Enterococcus faecalis.
 OS US2005058985-A1.
 XX
 PN

XX 17-MAR-2005.
 PD 12-SEP-2003; 2003US-00661094.
 PF 12-SEP-2003; 2003US-00661094.
 XX 12-SEP-2003; 2003US-00661094.
 PR (DODG/) DODGSON K J.
 PA Dodgson KJ;
 PI WPI; 2005-222218/23.
 XX
 DR
 PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
 PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
 PT and/or vanB-specific oligonucleotide probes or primers.
 PS Example 1; SEQ ID NO 16; 33pp; English.
 XX
 CC The invention relates to a method for detecting vancomycin resistance
 CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
 CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
 CC probe or primer, and detecting or determining the presence or amount of
 CC hybrid formation or amplified nucleic acid. Also described: (1) an
 CC oligonucleotide composition comprising a first oligonucleotide comprising
 CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
 CC 898-917 of the vanA gene, or its complement or portion, or an
 CC oligonucleotide comprising sequences substantially corresponding to
 CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
 CC complement or portion, where the oligonucleotide hybridizes under
 CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
 CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
 CC vanB gene in a test sample, comprising the oligonucleotide mentioned
 CC above. The method and kit are useful for detecting and/or amplifying
 CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
 CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
 CC They may also be used in other industrial purposes, such as for quality
 CC control of food, water, pharmaceutical products or other products
 CC requiring microbiological control. The present sequence represents an
 CC Enterococcus faecalis vanB nucleotide sequence from the present
 CC invention.
 CC
 SQ Sequence 783 BP; 215 A; 166 C; 223 G; 179 T; 0 U; 0 Other;
 Query Match 76.3%; Score 20.6; DB 14; Length 783;
 Best Local Similarity 85.2%; Pred. No. 24;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
 Db 392 CCTACCTGTTGTAAGCCGCGC 418
 RESULT 35
 ID AAH01126 standard; DNA; 801 BP.
 XX AAH01126;
 XX
 DT 24-JUL-2001 (first entry)
 XX
 DE Enterococcus faecium nucleotide sequence SEQ ID NO:1117.
 XX
 KM Species specific; genus specific; family specific; probe; detection;
 KM identification; algal; archaeal; bacterial; fungal; parasitic;
 KM microorganism; diagnosis; translation elongation factor Tu; toxin;
 KM translation elongation factor G; RecA recombinase; resistance;
 KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KM primer; ds.
 XX Enterococcus faecium.
 OS WO200123604-A2.
 XX
 PN

XX 05-APR-2001.
PD 28-SEP-2000; 2000MO-CA001150.
XX 28-SEP-1999; 99CA-02283458.
XX 19-MAY-2000; 2000CA-02307010.
XX (INPR-) INFECTIO DIAGNOSTIC (IDT) INC.
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX WPI; 2001-24506/25.
DR Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitic species in a test sample.
XX Disclosure; Page 1027; 1580pp; English.
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitic
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitic species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 801 BP; 215 A; 169 C; 235 G; 182 T; 0 U; 0 Other;
XX
Query Match 76.3%; Score 20.6; DB 4; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
DB 389 CCTACCTGTCTTGTGTAAGCGGCGAC 415
XX
RESULT 36
ADY59937/c
ID ADY59937 standard; DNA; 801 BP.
XX
AC ADY59937;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecium vanB DNA sequence SEQ ID NO:11.
XX
KM DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS Enterococcus faecium.
XX
PN US2005058985-A1.

XX 17-MAR-2005.
PD 12-SEP-2003; 2003US-00661094.
XX 12-SEP-2003; 2003US-00661094.
XX 12-SEP-2003; 2003US-00661094.
XX (DODG/) DODGSON K J.
XX Dodgson KJ;
XX WPI; 2005-222218/23.
XX
DR Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX Example 1; SEQ ID NO 11; 33pp; English.
XX
PS The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contracting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus)
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ Sequence 801 BP; 181 A; 226 C; 169 G; 225 T; 0 U; 0 Other;
XX
Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
DB 413 CCTACCTGTCTTGTGTAAGCGGCGAC 387
XX
RESULT 37
ADY59940/c
ID ADY59940 standard; DNA; 801 BP.
XX
AC ADY59940;
XX
DT 02-JUN-2005 (first entry)
XX
DE Enterococcus faecium vanB DNA sequence SEQ ID NO:14.
XX
KM DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX
OS Enterococcus faecium.
XX
PN US2005058985-A1.
XX
PD 17-MAR-2005.
XX
PD 12-SEP-2003; 2003US-00661094.
XX
PF 12-SEP-2003; 2003US-00661094.
XX

XX (DODG/) DODGSON K J.
 XX
 PA Dodgson KJ;
 PI
 XX WPI, 2005-222218/23.
 DR
 XX
 PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
 PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
 PT and/or vanB-specific oligonucleotide probes or primers.
 XX
 PS Example 1; SEQ ID NO 14; 33pp; English.
 XX
 CC The invention relates to a method for detecting vancomycin resistance
 CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
 CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
 CC probe or primer, and detecting or determining the presence or amount of
 CC hybrid formation or amplified nucleic acid. Also described: (1) an
 CC oligonucleotide composition comprising a first oligonucleotide comprising
 CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
 CC 898-917 of the vanA gene, or its complement or portion, or an
 CC oligonucleotide comprising sequences substantially corresponding to
 CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
 CC complement or portion, where the oligonucleotide hybridizes under
 CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
 CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
 CC vanB gene in a test sample, comprising the oligonucleotide mentioned
 CC above. The method and kit are useful for detecting and/or amplifying
 CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
 CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
 CC They may also be used in other industrial purposes, such as for quality
 CC control of food, water, pharmaceutical products or other products
 CC requiring microbiological control. The present sequence represents an
 CC Enterococcus faecium vanB nucleotide sequence from the present invention.
 XX
 SQ Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other;
 XX
 QY Query Match 76.3%; Score 20.6; DB 14; Length 801;
 Best Local Similarity 85.2%; Pred. No. 25;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 Db 1 CCGATCCTGTTTGTGTAAGCCGCGC 27
 413 CCGATCCTGTTTGTGTAAGCCGCGCAC 387
 XX
 RESULT 38
 ADY59943/c
 ID ADY59943 standard; DNA; 801 BP.
 XX
 AC ADY59943;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Consensus vanB DNA sequence SEQ ID NO:14.
 XX
 KM DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
 XX
 OS Enterococcus faecium.
 OS Enterococcus faecalis.
 OS Synthetic.
 XX
 PN US2005058985-A1.
 XX
 PD 17-MAR-2005.
 XX
 PF 12-SEP-2003; 2003US-00661094.
 XX
 PR 12-SEP-2003; 2003US-00661094.
 XX
 PA (DODG/) DODGSON K J.
 XX
 PI Dodgson KJ;

XX WPI, 2005-222218/23.
 DR
 XX
 PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
 PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
 PT and/or vanB-specific oligonucleotide probes or primers.
 XX
 PS Example 1; SEQ ID NO 17; 33pp; English.
 XX
 CC The invention relates to a method for detecting vancomycin resistance
 CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
 CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
 CC probe or primer, and detecting or determining the presence or amount of
 CC hybrid formation or amplified nucleic acid. Also described: (1) an
 CC oligonucleotide composition comprising a first oligonucleotide comprising
 CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
 CC 898-917 of the vanA gene, or its complement or portion, or an
 CC oligonucleotide comprising sequences substantially corresponding to
 CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
 CC complement or portion, where the oligonucleotide hybridizes under
 CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
 CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
 CC vanB gene in a test sample, comprising the oligonucleotide mentioned
 CC above. The method and kit are useful for detecting and/or amplifying
 CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
 CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
 CC They may also be used in other industrial purposes, such as for quality
 CC control of food, water, pharmaceutical products or other products
 CC requiring microbiological control. The present sequence represents a
 CC consensus vanB nucleotide sequence from the present invention.
 XX
 SQ Sequence 801 BP; 181 A; 235 C; 169 G; 216 T; 0 U; 0 Other;
 XX
 QY Query Match 76.3%; Score 20.6; DB 14; Length 801;
 Best Local Similarity 85.2%; Pred. No. 25;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 Db 1 CCGATCCTGTTTGTGTAAGCCGCGC 27
 413 CCGATCCTGTTTGTGTAAGCCGCGCAC 387
 XX
 RESULT 39
 ADY59939/c
 ID ADY59939 standard; DNA; 801 BP.
 XX
 AC ADY59939;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Enterococcus faecium vanB DNA sequence SEQ ID NO:13.
 XX
 KM DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
 XX
 OS Enterococcus faecium.
 OS Enterococcus faecalis.
 OS Synthetic.
 XX
 PN US2005058985-A1.
 XX
 PD 17-MAR-2005.
 XX
 PF 12-SEP-2003; 2003US-00661094.
 XX
 PR 12-SEP-2003; 2003US-00661094.
 XX
 PA (DODG/) DODGSON K J.
 XX
 PI Dodgson KJ;
 XX
 WPI, 2005-222218/23.
 DR
 XX
 PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
 PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
 PT and/or vanB-specific oligonucleotide probes or primers.

XX Example 1; SEQ ID NO 13; 33bp; English.
PS
XX The invention relates to a method for detecting vancomycin resistance
CC gene vana and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vana- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vana gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vana or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vana gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vana and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
CC
XX
SQ Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAACCGCGCGC 27
DB 413 CCTACCTGTCTTGTGTAAGCGCGCAC 387
RESULT 40
ADYS9936/C
XX ID ADYS9936 standard; DNA; 801 BP.
XX AC ADYS9936;
XX
XX 02-JUN-2005 (first entry)
XX
XX Enterococcus faecium vanB DNA sequence SEQ ID NO:10.
XX DE
XX DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX KM
XX Enterococcus faecium.
XX OS
XX US2005058985-A1.
XX PN
XX 17-MAR-2005.
XX PD
XX 12-SEP-2003; 2003US-00661094.
XX PF
XX 12-SEP-2003; 2003US-00661094.
XX PR
XX (DODG/) DODGSON K J.
XX PA
XX Dodgson KJ;
XX PI
XX WPI; 2005-222218/23.
XX DR
XX
XX Detecting vana and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vana-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
XX Example 1; SEQ ID NO 10; 33bp; English.
PS
XX The invention relates to a method for detecting vancomycin resistance
CC gene vana and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vana- and/or vanB-specific oligonucleotide

CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vana gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vana or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vana gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vana and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
CC
XX
SQ Sequence 801 BP; 182 A; 235 C; 169 G; 215 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAACCGCGCGC 27
DB 413 CCTACCTGTCTTGTGTAAGCGCGCAC 387
Search completed: April 9, 2006, 06:41:33
Job time : 381.134 secs

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